Supplementary Information

Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals

Supplementary Note

Power calculations

Power estimation was performed in R (https://genome.sph.umich.edu/wiki/Power_Calculations:_Quantitative_Traits) and the additive variance formula came from Falconer D.S.[1]. With our Pan-Ancestry meta-analysis of up to 1,318,884 individuals, we have 80% power to detect association with a variant with H2 of 0.003%, which corresponds to a variant with MAF of 0.01 and effect size of 0.039, or a variant with MAF=0.05 and effect size of 0.018 (Supplementary Figure 2). The effect sizes in our analyses are in terms of standard deviation (SD) units.

Study-level analyses

Each contributing Stage 1 study conducted exome-wide analyses of inverse normal transformed SBP, DBP and PP as well as HTN. The analyses of the transformed traits were performed to minimize sensitivity to deviations from normality in the analysis and discovery of rare variants. The residuals from the null model obtained after regressing the medication-adjusted trait on the covariates (age, age^2, sex, BMI, principal components [PCs] to adjust for population stratification, in addition to any study-specific covariates) within a linear regression model, were ranked and inverse normalized. These normalized residuals were used to test trait-SNV associations using RMW[2] version 4.13.3 by all studies except four studies which used SNPTEST v2.5.1 (EPIC-Norfolk, Fenland-GWAS, Fenland-OMICS and EPIC-InterAct-GWAS: Supplementary Table 23), assuming an additive allelic effects model and two-sided tests with a linear or linear mixed regression model. All SNVs that passed quality control were analysed for association with the continuous traits without any further filtering by MAF. For HTN, only SNVs with a minimum minor allele count (MAC) of 10 were analysed.

Quality control of study level data was performed centrally and included plots comparing the inverse of the standard error versus square root of sample size for each study to detect any issues with trait transformations, and checks for concordant MAFs across studies. Five studies (CARDIA, NFBC1986, ALSPAC_Mothers, WHI: African Americans and WHI: Europeans) were excluded from analyses of HTN as they have insufficient numbers of hypertensive cases to provide reliable estimates. We did not observe excessively high inflation in study level data (maximum lambda=1.06, 1.07, 1.14 for SBP, DBP, PP, respectively).

EAWAS Study design

We curated a list of 362 BP-associated loci that were known at the time of the analyses and conservatively defined known loci using both distance (±500kb) and LD such that variants outside of the known loci had $r^2 < 0.1$ (in 1000 Genomes EUR) with the previously reported variants (Methods; Supplementary Table 1). Single variant association summaries for 382 SNVs with $P<5x10^{-8}$ (derived from two-sided tests) outside of these regions (Stage 1) was requested from MVP, deCODE and GENOA. Results obtained from MVP, deCODE and GENOA was meta-analysed. Meta-analyses of Stage 1 and the results from meta-analyses of MVP, deCODE and GENOA was performed and any variant with *P*-value$<5x10^{-8}$ and consistent direction of effects with no evidence for heterogeneity were considered new.

Three hundred and forty-four SNVs (200 genomic regions; eight rare SNVs, 25 low-frequency SNVs; Methods) of the 382 BP-associated SNVs (91%) were associated with one or more BP traits at $P<5x10^{-8}$ in the combined EUR (Stage 2) meta-analyses involving up to ~1.165 million individuals (Table 1, Supplementary Table 2, Figure 2). An additional seven SNVs from seven genomic regions were only genome-wide significant in the PA (Stage 2) meta-analyses of ~1.3 million individuals (Supplementary Table 2), bringing the total number of BP-associated SNVs in Stage 2 to 355. Of the novel EUR BP-associated SNVs, 41 (30 loci; three rare SNVs, four low-frequency SNVs) were associated with an additional BP trait in the PA meta-analyses in addition to the EUR associated trait. All the associations had consistent directions of effect across Stage 1 and also across Stage 2 and no evidence of heterogeneity ($P>0.0001$; Supplementary Table 2).

Quality Control of novel BP-associated variants from EAWAS and RV-GWAS

We adopted a single discovery-stage meta-analysis study design for both the EAWAS and RV-GWAS primarily for reasons of statistical power. The data request studies were not statistically powered on their own to detect the effects of the subset of SNVs we selected for data request from MVP/deCODE/GENOA (EAWAS) or MVP (RV-GWAS) since these studies involved only around half the samples of the discovery. For a replication study, a sample size similar to, or larger than that used for the discovery, is required to have sufficient statistical power. In the absence of a well powered replication dataset, we have taken exhaustive measures to ensure the robustness of our findings.

We ensured that novel BP-associated variants that we claim were not driven by a single study. All reported variants had data from ≥ 19 studies in the Stage 1 EAWAS and 2 studies in the RV-GWAS, reducing the likelihood of a false association. In addition, all the novel BP-associated variants we report had consistent directions of effect in the Stage 1 studies and the data request studies (MVP+deCODE+GENOA for EAWAS, MVP alone for RV-GWAS). We verify the assumption of the fixed effects meta-analysis model, we ensured there was no evidence of heterogeneity across the effect estimates from contributing studies. In addition, we performed random effects meta-analysis (Han and Eskin's AJHG 2011 Random Effects Model) of novel BP-associated variants to minimise false discoveries due to study heterogeneity. The below plot (Supplementary Figure 3a) compares the $-\log_{10}$(*P*-values) from the fixed effect and random effects meta-analyses for all the variants in the EAWAS for which data were requested in the look up studies (see Supplementary Table 2a). There is strong concordance, suggesting that a fixed effects meta-analysis model is appropriate.

To ensure that the frequency of variants are not a result of inaccurate clustering/genotype calling, we confirmed that the allele frequencies were in the expected range by comparing the allele frequencies between Stage 1 and the data request studies (MVP+deCODE+GENOA for the EAWAS and MVP alone for RV-GWAS, Supplementary Figure 3b). In addition, we compared the allele frequencies to those in the reference datasets (gnomAD, UCSC, and 1000 Genomes). Allele frequencies were plotted to check for consistency and those not consistent were removed *e.g.* rs7775698. The plot below shows the comparison of MAFs of novel variants in EAWAS between Stage 1 and MVP+deCODE+GENOA.

Where variants were only available in a small number of studies, we checked the cluster plots of the studies involved and such variants as rs201702041, rs200510006, rs142360750 and rs143226982 that were poorly clustered in the PROMIS study were removed.

Within UK Biobank we performed our own QC for the genotyped variants rather than using the QC'd data as provided by UK Biobank, as we were specifically interested in the rare variants and knew that these were most vulnerable to clustering errors. Also described in detail within the section: "UK Biobank specific analyses" in this document. For the RV-GWAS and the FINEMAP analyses of UK Biobank we were able to perform additional checks for some of the variants. We compared the minor allele frequencies of the variants genotyped by arrays or imputed with those genotyped using whole exome sequencing. For the three novel BP-associated variants we identified in UK Biobank (rather than the EAWAS), the MAF was consistent between the imputed and WES data, suggesting the genotyping was robust.

Variants 1: Chromosome: 1; Position: 198,222,215
rsID: rs55833332
MAF in WES (both versions of calling/QC): 0.00747
MAF for the imputed variant in UKBB: 0.00816
MAF of variant in gnomAD v2.1.1 (for reference): 0.006475 (exomes), 0.008991 (genomes) and 0.009749 (European non-Finnish)

Variant 2: Chromosome: 20; Position: 61,050,522
rsID: rs200383755
MAF in WES (both versions of calling/QC): 0.00680
MAF for the imputed variant in UKBB: 0.00601
MAF of variant in gnomAD v2.1.1 (for reference): 0.003412 (exomes), 0.003479 (genomes) and 0.005443 (European non-Finnish)

Variant 3 (was imputed): Chromosome: 14; Position: 100,143,685
rsID: rs149250178
MAF in WES (both versions of calling/QC): 0.00020
MAF for the imputed variant in UKBB: 0.00036
MAF of variant in gnomAD v2.1.1 (for reference): no variant (exomes), 0.003479 (genomes) and 0.001104 (European non-Finnish)

We compared the minor allele frequency (MAF) calculated using genotyped genotypes and imputed genotypes of the rare variants both genotyped and imputed in UKBB. We looked at this distribution as a function of the INFO score and identified that the MAF of the imputed variants with INFO>0.3 had an almost perfect correlation (ρ>0.9998) with the MAF of genotyped variants. Based on this comparison we only analysed rare variants with an INFO>0.3 in UKBB. We checked imputation quality for any BP-associated variant that was claimed and imputed. All variants we claim had imputation info score >0.8 in all Stage 1 studies.

Associations of previously reported variants in the Stage 1 EAWAS and UKBB

Of the 362 BP-associated loci reported prior to our analyses (*i.e.* pre-2018; Methods; Supplementary Table 1), 291 (80%) had one or more genome-wide significant associations in our UKBB GWAS that were in LD with the previously reported variant and 124 were genome-wide significant in the EAWAS. We confirmed 332 known loci at $P \leq 5x10^{-5}$ and 344 (95%) were nominally significant ($P \leq 0.05$).

Comparison of conditional analyses in the EAWAS and UKBB GWAS

For eight of the known regions in Table 2 the common BP-associated SNVs were not available on Exome array, but independently associated rare/low-frequency variants had been identified. We therefore verified that these associations were valid using the dense genomic coverage in UKBB. At *NOX4*, *ZFAT*, *GEM*, *MYO1C* and *LTBP4* the same variants (or proxies r^2>0.9) were identified with FINEMAP in UKBB (Table 3) as with GCTA for the EAWAS (Table 2). At *GEM* and *NOX4* two rare BP-associated SNVs were identified in both genes in addition to the previously reported common variant associations (Table 3; Supplementary Table 8). At *FBXL19*, a rare missense variant was independent of the common variant signal in the EAWAS, (Table 2, Supplementary Table 8) while in the FINEMAP analyses in UKBB, an intron variant in *STX4* was in LD (r^2=0.88) with the *FBXL19* missense variant. (A second rare SNV, rs2234710, upstream of *BCL7C*, was independent of the *STX4* and common variant associations at this locus, in UKBB.) At *FOXS1*, a rare missense variant was identified as the top association in the EAWAS, while in the FINEMAP UKBB analyses an intronic variant in *MYLK2*, which is in LD (r^2=1 in 1000 genomes EUR) with the *FOXS1* variant was identified, and although the *FOXS1* SNV is a more attractive candidate causal variant as it is missense, *MYLK2* is an attractive candidate gene as it is targeted by the drug Fostamatinib, which is used for the treatment of chronic immune thrombocytopenia and hypertension is reported as a side effect of Fostamatinib. Therefore it is likely that the rare/low-frequency associations at these loci are valid and independent of the established common variant associations.

Annotation of BP-associated variants

We used extensive bioinformatic approaches to collate functional annotations of variants and genes within the novel and known BP-associated loci. For variants, we used VEP[3] to obtain comprehensive functional characterization of sentinel and conditionally independent variants and their proxies ($r^2 \geq 0.8$; using the same approach as for locus definitions) including gene location, conservation and amino acid substitution.

Across all 589 BP loci considered, 45% of the independent BP-associated rare variants were coding, while amongst the common variants, 20% were coding, in part reflecting the exome-centric design of the EAWAS. Twenty-one rare and 43 low-frequency variants were within regulatory elements including enhancers, promoters, CTCF binding sites, transcription factor binding sites and open chromatin regions highlighting genetic control of BP levels through gene expression.

Gene-based association tests sensitivity analyses

Amongst the genes that map to our newly identified BP-associated loci, ten from the EAWAS (*SCMH1*, *FILIP1L*, *CEP97*, *G6PC2*, *PHC3*, *HAUS6*, *PLCB3*, *TBX5*, *SOS2*, *NEK9*) and four from the RV-GWAS (*NEK7*, *PHC3*, *TBX5*, *GATA5*) were associated with BP ($P<2.5x10^{-6}$). Analyses conditional on the top SNV in the gene showed that the associations were attributable to a single rare variant identified in the single variant analyses and not likely to be due to multiple rare SNVs (Supplementary Table 9).

We tested the genes that mapped to the 362 previously reported BP loci. In the EAWAS, 21 genes within known loci, were associated with BP ($P<2.5x10^{-6}$; Supplementary Table 9) and ten genes (two not in the EAWAS list, *ZNF646* and *COL17A1*) were associated in the RV-GWAS ($P<2.5x10^{-6}$; Supplementary Table 9). Analyses conditional on the top SNV in the gene, showed that six of these gene associations were due to multiple rare SNV associations (*GEM*, *NPR1*, *DBH*, *COL21A1*, *NOX4* and *AGT*: SKAT conditional $P<1x10^{-4}$; Supplementary Table 9). To test whether the associations were due to LD with known common BP-associated variants, we also performed SKAT tests conditional on the known common variants in the individual loci. Five of the genes, *NPR1*, *DBH*, *COL21A1*, *NOX4*, *GEM*, were associated with BP independently of both the common variant associations and the top SNV in the gene ($P\leq1x10^{-5}$; Supplementary Table 9) confirming the findings in the single variant conditional analyses (Supplementary Table 8).

To assess sensitivity to the MAF threshold, we repeated the gene-based tests using a MAF<0.05 threshold. No genes with multiple rare/low-frequency SNVs were identified outside of known or novel regions (conditional SKAT $P>0.0001$; Supplementary Table 9). Of the 27 genes that were associated in the novel loci ($P<2.5x10^{-6}$), the association at *PLCB3* with DBP was due to multiple DBP-associated SNVs ($P=2.63x10^{-6}$; Supplementary Table 9) consistent with the conditional single variant analyses that identified one rare and one low-frequency variant associated in this gene (Supplementary Table 8). Of the 67 genes associated in known regions, nine (*NPR1*, *DBH*, *COL21A1*, *NOX4*, *CEP120*, *LARP4*, *PLCE1*, *NOS3* and *TBC1D32*) were due to multiple SNVs, and the associations with *NPR1*, *COL21A1*, and *CEP120* were not due to common variant associations (conditional SKAT $P<1x10^{-5}$; Supplementary Table 9, 10). In total, seven genes, one in a novel region (*PLCB3*) and six in known regions (*NPR1*, *DBH*, *COL21A1*, *NOX4*, *GEM* and *CEP120*) were implicated in BP regulation with multiple SNVs associated in the genes that were not due to LD with established common SNV-BP associations.

Rare variant gene-set enrichment analyses

Lists of genes representing various pathways and biological processes were constructed from the following sources: GO (download from http://geneontology.org/ on December 9, 2018, using the files go-basic.obo and goa_human.gaf), GTEX (download from https://gtexportal.org on December 9, 2018, using the file GTEx_Analysis_2016-01-15_v7_RNASeQCv1.1.8_gene_median_tpm.gct.gz), KEGG (downloaded from ftp.pathways.jp on December 9, 2018 using the files hsa.list and map_title.tab), MGI (downloaded from http://www.informatics.jax.org downloads/reports on December 9, 2018, using the files MPheno_OBO.ontology.obo, HMD_HumanPhenotype.rpt and MGI_PhenoGenoMP.rpt) and Orphanet (downloaded from http://www.orphadata.org/data/ORDO/ on December 9, 2018, using the files ordo.owl). For GTEx, a gene set for a tissue was defined as the set of all genes with highest expression in that tissue. In the cases of the ontologies (GO, MGI, Orpha) gene sets were constructed by first collecting the genes annotated to each specific node and then rolling these annotations up to each parent node recursively to the top of the ontology. For the MGI data the mouse to human orthology mappings provided in the source files were used. All gene references were mapped to entrez IDs using Homo_sapiens.gene_info file obtained from ftp://ftp.ncbi.nih.gov/gene/DATA/GENE_INFO/Mammalia. Genes not listed as "protein-coding" genes in entrez genes were omitted, as were genes with no chromosomal mappings in the hg38 reference genome assembly. Gene sets with only a single gene were eliminated from further consideration.

We tested whether genes near rare BP-associated SNVs were enriched in gene sets from Gene Ontology (GO), KEGG, Mouse Genome Informatics (MGI) and Orphanet (Methods; Supplementary Table 4). These (rare variant) genes from both known and novel loci were enriched in BP-related pathways (Bonferroni adjusted $P<0.05$, Methods; Supplementary Table 13) including "regulation of blood vessel size" (GO) and "renin secretion" (KEGG). Genes implicated by rare SNVs at known loci were enriched in "tissue remodeling" (GO) and "artery aorta" (GO). Genes implicated by rare SNVs at new BP-loci were enriched in rare circulatory system diseases (that include hypertension and rare renal diseases) in Orphanet.

Drug target prioritisation

The list of genes nearby the low-frequency and rare variant associations in both novel and previously identified loci (Supplementary Table 12) were cross-referenced in the list of "druggable" genes from Finnan et al.[4]. Those that were potentially targetable were queried in Open Targets (opentargets.org) and drugbank (www.drugbank.ca/) to assess whether there were pre-existing molecules for these genes.

Information on some new BP genes

Below is provided some information on some interesting genes harbouring or neighbouring new BP-associated rare/low-frequency variants.

ZFHX3

The low frequency missense variant rs62051555 (p.Gln2014His), located in exon eight of the transcription factor, zinc finger homeobox 3 (*ZFHX3*), is associated with increased levels of SBP and PP. Interestingly, *ZFHX3* plays a role in the left-right patterning of cardiac atria during development, with changed expression of genes important for sidedness [5]. Mice with cardiac-restricted knockdown of *ZFHX3* have cardiomyopathy, impaired left ventricular function, atrial enlargement, altered atrial electrophysiology properties (increased conduction velocity) [5] and abnormalities in calcium homeostasis [6,5]. They also have severely dilated and fibrosed atria with a large mass consistent with thrombus and a significantly shorter life span compared to control animals [5]. The above abnormalities can increase susceptibility to atrial fibrillation (AF) [5]. *ZFHX3* has been reported multiple times to be associated with AF [7,8,9,10,11,12], a major risk factor for cardioembolic stroke[13] [14,15]. The association between AF and an increased risk for cardiovascular morbidity and mortality cannot be explained by thromboembolism alone, and patients with AF have increased beat-to-beat BP variability, which may adversely affect vascular structure and function [16], which can potentially influence BP.

LAMA5

Two low-frequency missense variants, rs11699758 (p.Val1757Ile) and rs13039398 (p.Arg1667Trp), residing in *LAMA5*, are associated with decreased SBP and PP. *LAMA5* encodes an extracellular matrix laminin α5 chain. Laminins are a group of α/β/γ glycoprotein heterotrimers, which constitute the main noncollagenous component of basement membranes [17]. Laminin α5 plays an important role in embryogenesis, and *Lama5*-/- mice embryos do not survive until birth [17]. Particularly, laminin heterotrimers containing laminin α5 chain are involved in glomerulogenesis, and are essential for the formation of the glomerular basement membrane, so that *Lama5*-/- embryos have failed vascularization of glomeruli in kidneys and even present with kidney agenesis [18].

Moreover, endothelial cell basement membrane laminin α5 is required for a normal shear response by resistance arteries [19]. The loss of laminin α5 from endothelial basement membranes in Tek-Cre::*Lama5*-/- mice results in an almost complete elimination of dilation in response to increased shear stress, which correlates with decreased endothelial cell cortical stiffness, decreased size of integrin beta1-positive/vinculin-positive focal adhesions and decreased junctional association of actin–myosin II [19]. *In vitro* experiments suggest that arterial endothelial cells directly bind to laminin α5/β1/γ1 via β1 integrins and that this binding increases VE-cadherin stabilization at cell-cell junctions, required for an adequate shear response [19].

LAMA5 is also a target of a therapy under investigation for treatment of stroke (Supplementary Table 14).

HSPA4

The missense variant of *HSPA4* (rs61755724, p.Ala159Thr) is associated with increase in DBP. Heat shock protein HSPA4 is a member of the HSP110 family and acts as a nucleotide exchange factor of HSP70 chaperones [20]. Upregulated expression of Hspa4 is observed in murine hearts exposed to

pressure overload and in failing human hearts [20]. Furthermore, *Hspa4-/-* mice developed cardiac concentric hypertrophy and fibrosis with elevated expression levels of hypertrophic markers and an accumulation of polyubiquitinated proteins in neonatal hearts, suggesting that *Hspa4-/-* plays a role in protein quality control [20].

MCL1

The missense variant rs11580946 (p.Ala227Val), belonging to apoptosis regulator MCL1, is associated with decreased levels of SBP and PP. MCL1 participates in survival of haematopoietic stem cells [21], progenitor cells, effector lymphocytes and cardiomyocytes [22]. Given its role in cell survival, MCL1 is a drug target for cancer-related phenotypes, with the small molecule inhibitor (antagonist) currently in 1 phase II trials and also for emergency treatment of acute angle-closure glaucoma and other conditions in which rapid reduction in intraocular pressure and vitreous volume is indicated (Supplementary Table 14). Cardiac-specific ablation of *Mcl-1* in mice results in a rapidly fatal dilated cardiomyopathy, preceded by loss of myofibrils and cardiac contractility, abnormal mitochondria ultrastructure, defective mitochondrial respiration, and impaired autophagy [23].

TBX5

The newly identified rare variant rs77357563 (p.Asp111Tyr; predicted deleterious by SIFT) in *TBX5*, is adjacent to the known *TBX3* region[24-26] and highlights *TBX5* as an additional candidate gene. *TBX5* is essential for normal cardiac development. Mutations in *TBX5* are known to cause various congenital heart diseases[27] and arrhythmias including Holt Oram syndrome and are associated with atrial fibrillation[28].

TGFB2

We observed rare variants in both intergenic and intronic regions, one rare intergenic variant rs12135454 is located near *TGFB2*. Prior work has indicated the TGFβ pathway as important in the genetics of BP traits[29]. Mutations in *TGFB2* cause Loeys-Dietz syndrome 4, a condition which includes aortic aneurysm, bicuspid aortic valve and arterial tortuosity.[30]

Mendelian Randomisation to assess the effect of metabolites on BP

We tested for pleiotropic effects of the IVs used for the 3-methylglutarylcarnitine(2) using two models. Firstly, we included any of the 14 metabolites in the analyses that shared at least one IV with 3-methylglutarylcarnitine(2) in a multi-variable MR model (three metabolites in total). Secondly, we included glycine in a multi-variable MR model with 3-methylglutarylcarnitine(2) as these two metabolites shared several IVs but glycine was not in our list of 14 metabolites analysed and we have recently shown that glycine is causal for BP[31]. 3-methylglutarylcarnitine(2) was consistently and significantly associated with DBP ($P < 0.05$) in the multi-variable MR models. Notably, we found that 3-methylglutarylcarnitine(2) was independently associated with DBP adjusting for the effect of glycine. Sensitivity analysis from multi-variable MR-Egger showed little evidence that the Egger intercept was deviated from zero for both models ($P_{\text{intercept}} > 0.01$).

We found genetically determined 3-methylglutarycarnitine (2) was predictive of DBP in both univariable and multivariable MR analyses (Supplementary Table 16). 3-methylglutarylcarnitine belongs to the class of organic compounds known as acyl carnitines involved in long-chain fatty acid metabolism in mitochondria and in leucine metabolism. It is a diagnostic metabolite of 3-hydroxy-3-methylglutaryl-coenzyme A lyase deficiency, an inborn error of metabolism in which the body cannot process leucine or generate ketones[32], with dilated cardiomyopathy as a complication[33]. Leucine has been shown to increase hypothalamic mTORC1 leading to an increase in BP[34]. A prospective clinical study also found that 3-methylglutarycarnitine was significantly lower in maternal first-trimester serum of fetal congenital heart defects (CHDs) than healthy controls[35].

Kidney expression data

Datasets, expression and SNP genotyping

The *cis*-eQTL meta-analysis was carried out using data from two projects: TRANScriptome of renaL humAn TissuE (TRANSLATE) Study (N=186) and The Cancer Genome Atlas (TCGA) study (N=99). The same quality control filters, data processing and analyses methods were applied to both datasets. Gene expression was quantified in terms of transcripts per million (TPM) using Kallisto[36]. Outlier samples were removed based on a statistic described in Wright *et al*. [37] or based on pairwise correlation between samples, where samples with median correlation <0.8 were excluded as per 't Hoen *et al*. [38]. Only genes on autosomal chromosomes were selected for the analysis. Gene expression threshold was set at TPM>0.1 in at least 20% of samples within each study/sequencing batch and read counts ≥ 6. A gene was also removed if its interquartile range was zero. Only genes that passed all of the above RNA-seq quality control filters in both studies were used in the analysis.

Gene-level TPM values were normalised as follows. First, $\log_2$ of TPM values were normalised across samples using robust quantile normalisation. Second, the normalised gene expression values were transformed using rank-based inverse normal transformation. Third, to account for hidden variation in RNA-seq data due to technical processing (such as batch effects or sample processing in pre-sequencing stage), we used probabilistic estimation of expression residuals (PEER) method[39] and estimated 30 hidden factors for TRANSLATE Study and 15 for TCGA. The numbers of hidden factors were chosen based on sample sizes of each dataset as recommended in GTEx eQTL analyses[40,41].

In TRANSLATE Study, genotyping was done using Infinium HumanCoreExome-24 BeadChip arrays and the allele calls were made using Genome Studio. In TCGA, genotyping was done using Affymetrix Genome-Wide Human SNP Array 6.0 and the allele calls were made using Birdseed. The following quality control filters were applied to genotype data. Samples were excluded if their genotyping rate was <95%, their heterozygosity rate was outside ± 3 standard deviations from the mean, they had cryptic relatedness with other individuals, were of non-white European genetic ancestry or had discordant sex information (inconsistency between declared and genotyped sex). Genetic variants were excluded if their genotyping rate was <95%, they mapped to Y chromosome or mitochondrial DNA, they had ambiguous chromosomal location, they violated Hardy-Weinberg equilibrium (HWE) (P<0.001) or if their minor allele frequency (MAF) was <5%.

Genotype imputation was conducted using *minimac3*[42] with Haplotype Reference Consortium data as the reference panel. The imputation was performed on Michigan Imputation Server[42]. Post-imputation, we excluded duplicate variants, non-SNPs, variants with low imputation coefficient (R^2<0.4), low frequency variants (MAF<5%) and variants that violated HWE ($P<10^{-6}$).

Multiple linear regression was used to test association between gene expression and genotype and the estimated coefficients from both studies were meta-analysed using inverse-variance weighted fixed effects. For each gene, only those SNVs within 1Mb of the transcription start/stop sites (cis) were included in the analysis. Two thousand permutations were used to derive the empirical distribution of the smallest *P*-value for each gene, which then was used to adjust the observed smallest *P*-value for the gene. The correction for testing multiple genes was based on false discovery rate (FDR) applied to permutation-adjusted *P*-values (via Storey's method as implemented in the R package q-value) with a cut-off of 0.05. Furthermore, the thresholds for nominal *P*-values were derived using a global permutation-adjusted *P*-value closest to FDR of 0.05 and the empirical distributions determined using permutations.
The BP SNVs (N=358 at 214 loci, see Supplementary Table **1**b) were considered or proxies (r^2>0.8) if the sentinel SNV was not available. For reporting we only considered genes with FDR<0.05 and significant *cis*-eQTLs at $P<5\times10^{-8}$. If the BP-associated SNV and the eQTL were the same or in high LD (r^2>0.8), the BP SNV was reported as an eQTL

cis-eQTL meta-analysis
The association between gene expression and genotype was conducted using multiple linear regression with normalised gene expression as the dependent variable and genotype dosage, sex, top three genotype-derived principal components and the estimated hidden factors (30 for TRANSLATE Study and 15 for TCGA) as independent variables. The estimated coefficients from both studies were combined using inverse variance method. Only SNPs within 1Mb from the closest bound of a gene were considered. The correction for multiple testing for analysis of each gene with its in-*cis* SNPs was conducted using the permutation test, where the distribution of the smallest meta-combined P-value was determined using 2,000 permutations. At each permutation, the genotype sample labels were permuted but kept coupled with the sample labels of the top three genotype principal components for TRANSLATE Study data and TCGA data, separately. For each gene, the associations between its expression and its in-*cis* SNPs were re-estimated and the smallest meta-combined *P*-value recorded. Finally, for each gene the SNP with the smallest meta-combined P-value was identified and adjusted

using the corresponding empirical distribution of the smallest meta-combined P-values for that gene. False discovery rate was determined using q-values from the *qvalue* R package. The permutation corrected P-values were used for calculating the false discovery rate (FDR) with a cut-off of 5%.
A threshold for nominal meta-combined *P*-values for SNPs that did not have the smallest meta-combined *P*-values was calculated as follows. First, a global permutation-adjusted P-value, p_t, was chosen to be the permutation-adjusted P-value for the gene with FDR closets to 5%. Then for each gene, a threshold for meta-combined nominal P-values was chosen to be the probability of observing a value less than or equal to p_t using the gene's empirical distribution of the smallest meta-combined *P*-values.
In total, 16,333 genes with at least one in-*cis* SNP and 4,862,143 SNPs with at least one in-*cis* gene were used in the analysis, resulting in 60,984,484 models. After correction for multiple testing, 4,431 genes passed FDR 5% cut-off. There were 425,096 statistically significant gene-SNP pairs that passed nominal P-value cut-offs: 317,425 unique SNPs associated with 4,431 genes.

The BP SNVs (N= 358 at 214 loci, see Supplementary Table 1b) were considered or proxies (r^2>0.8) if the sentinel SNV was not available. For reporting we only considered genes passing the 5% FDR cut-off and significant *cis*-eQTL signal(s) at $P < 5 \times 10^{-8}$. We reviewed the results for the most strongly associated *cis*-eQTL for the corresponding transcript. If the BP SNV and the eQTL were the same or in high LD (r^2>0.7), the BP SNV was reported as an eQTL. The results are summarized in Supplementary Table 18.

Colocalisation of BP associations and eQTL

Colocalisation analyses using the common variant results identified 32 unique BP-associated loci where the new BP-associated variant colocalised with the eQTL for 54 unique genes in GTEx tissues highlighting potential candidate genes. Many of the novel BP variants in genes including those in *PHACTR1, TIE1, CTSK, LTBP1, CRIM1, TIPARP* that colocalised with gene expression in GTEx in specific cardiovascular tissues, are also associated with CVD related phenotypes[43-56]. *TIE1* is involved in angiopoietin function in vascular remodelling and inflammation[57]. In the mouse, mutations in *Tie1* cause many cardiovascular phenotypes including small heart development, abnormal vascular endothelial cell morphology, abnormal endocardium morphology and abnormal heart atrium morphology[47,58]. Together these observations make *TIE1* a plausible candidate gene. *Crim1* KST264/KST264 mice implicate Crim1 in the regulation of vascular endothelial growth factor-A activity during glomerular vascular development[55]. *Tiparp* negative mice have kidney defects, including defects in smooth muscle cell number and location[59].

Tissue and cell enrichment analyses using DEPICT

We used DEPICT (Data-driven Expression Prioritized Integration for Complex Traits) as a complementary enrichment analysis to (1) identify tissues and cells in which genes at novel and previously reported BP loci are highly expressed and 2) to test for enrichment in gene sets associated with biological annotations, which included molecular pathways and phenotype data from mouse knockout studies. Two analyses were performed one involved all BP variants reported previously for BP traits (that were genome-wide significant in our dataset; Supplementary Table 5, 8) and a second

set including all previously reported BP variants and variants at new loci, i.e. newly validated genome-wide significant SNVs (including the rare variants identified in the RV-GWAS) and any independent variants at these loci (Supplementary Tables 2, 3, 7). We report significant enrichments with a false discovery rate of 1%. We found the most significant enrichments were observed for the urogenital system (P=1.25x10^{-16}), cardiovascular system (P=2.01x10^{-13}) and endocrine system (P=1.78x10^{-11}) (Supplementary Table 13).

Enrichment of BP-associated SNVs in DNase I-hypersensitive sites

To investigate cell-type-specific enrichment within DNase I-hypersensitive sites we used FORGE, which tests for enrichment of SNVs within DNase I-hypersensitive sites in 299 cell types from the Epigenomics Roadmap Project and 125 cell lines from ENCODE[60]. All common and rare **non-coding** novel and conditionally independent validated variants from EAWAS, and SNVs from the RV-GWAS (all P<5.0x10^{-8}) were included (Supplementary Tables 2, 3, 7). BP-trait specific analyses were not performed. We supplemented this listing to include all novel rare, low frequency and common variants from FINEMAP (variants not in LD (r^2>0.6) with a previously reported BP SNV (851 variants; Supplementary Table 8). In total 1,055 variants were included in the input from which 37 that were not in 1000 genomes Phase I and 64 that were in LD (r2>0.8) with the data were excluded leaving 954 for analysis. Enrichment was calculated by taking the Bonferroni corrected P-values from a binomial test comparing overlap of the supplied SNPs with 100 background SNP sets.

Significant results (Bonferroni corrected P-value<0.01) were observed across 15 tissues (Supplementary Table 13) in the ENCODE dataset. The strongest enrichments were in blood vessels, heart, skin, connective tissue, lung and epithelium (Z-score >6). These enriched tissues are similar to those reported for common BP associated SNVs[29]. Testing for enrichment in the Epigenomics Roadmap project indicated striking enrichment of BP SNVs in fetal kidney and fetal lung tissues (renal pelvis, renal cortex, renal kidney and lung, Z score=300) and significant enrichment across a further 12 tissues (new Supplementary Table 13).

Phenome-wide associations of the new common SNV BP loci

To identify diseases and other intermediate phenotypes associated with the novel BP variants (Supplementary Tables 2, 3), we performed a lookup of sentinel and conditionally independent variants and their proxies (r^2≥0.8) against publicly available GWAS data using PhenoScanner[61]. A list of datasets queried is available on the Phenoscanner website. Results were filtered to include association with P<5x10^{-8} for common variants and P<1x10^{-4} for rare variants. Either the sentinel variant or the proxy with the smallest P-value for each trait was further investigated.
We also queried PhenoScanner for associations with publicly available eQTL and pQTL.

Two BP-associated loci were in high LD (r^2>0.8) with alcohol consumption variants. Variants at four new BP loci were in high LD with red blood cell trait associated SNVs, in particular haemoglobin, and one of these was also shared with iron traits (Figure 3). One locus was in LD with platelet traits and one with a plasminogen related trait. The new BP variants were also in high LD with variants associated with eye diseases for which hypertension is a risk factor: two with age-related macular

degeneration and two with exfoliation glaucoma. The BP associated variant in *CASC16* was shared with Parkinson's disease. Telomere length has also been linked to aging and a variant at the *MYNN* locus was in LD with a telomere length associated variant.

Colocalization of BP-associated SNVs with cardiometabolic traits in the EAWAS

To estimate the probability that BP shared the same causal variant with other CVD risk factors, we conducted a co-localisation analysis. Using GWAS results from CVD risk factors (BMI[62], HDL Cholesterol[63], LDL Cholesterol[63], Triglycerides[63], fasting glucose[64], type 2 diabetes[65] and CAD[66]), we first identified SNV-CVD risk factor associations at each of the novel BP-associated loci. Within each locus, we conducted a Bayesian test for co-localisation using all shared SNVs using the coloc package in R.[67] Assuming that 1 in 10,000 SNVs are likely to be causal for either test trait, we applied the default prior probabilities for a SNV being associated with trait one only (p1), trait two only (p2), and with both traits (p12), with p1 and p2 set to 0.0001 and p12 set to 0.00001.

High blood pressure is one of several risk factors that act in concert increase risk for cardiovascular disease (CVD). To explore the genetic relations between blood pressure and other CVD risk factors (obesity, elevated blood total cholesterol, low density lipoprotein cholesterol [LDL], and triglyceride levels, high density lipoprotein [HDL] cholesterol levels, and diabetes), we conducted colocalization analyses using our blood pressure genetic results in conjunction with summary GWAS of other risk factors (body mass index[68], LDL cholesterol[63], triglycerides[63], HDL cholesterol[63], fasting glucose[64], type 2 diabetes[65] and coronary artery disease (CAD)[66]) using the COLOC package[67] in R to determine whether the same causal variant at each locus was associated with both blood pressure and CVD risk factor (Methods). At a posterior probability of both traits colocalising (H4) >90% (Supplementary Table 21), we found that blood pressure (DBP, SBP, PP) shared associated SNVs with CAD on chromosome 6 (SLC29A1/RP11-344J7.4 locus) , chromosome 19 (APOE/APOC1/GIPR/QPCTL), chromosome 20 (KCNB1/B4GALT5), chromosome 21(AP000318.2); with lipids (HDL cholesterol , LDL cholesterol and triglycerides) on chromosome 1(CD164L2), chromosome 3 (LINC02029), chromosome 4 (PPP3CA and PDGFC), chromosome 5 (C5orf67), chromosome 6 (SLC29A1 and LINC01625), chromosome 7 (KLF14), chromosome 12 (BCL7A), chromosome 19 (ZC3H4); with BMI on chromosome 1(ZZZ3), chromosome 2 (ACMSD),chromosome 4(PPP3CA), chromosome 5 (RP11-6N13.1), chromosome 6 (FOXO3), chromosome 7(HIP1 and KLF14), chromosome 16(CNOT1), chromosome 19 (ZC3H4); with fasting glucose on chromosome 2 (SPC25/ABCB11/G6PC2), chromosome 11 (MTNR1B/SNRPGP16); and with type 2 diabetes on chromosome 3 (PPARG) (Supplementary Figure 4).

Mendelian Randomisation (MR) analyses of CVDs

We applied Mendelian randomisation (MR) to estimate the effects of blood pressure on CVD traits in a two-sample MR framework. The MR approach was based on the following assumption: (i) the genetic variants used as instrumental variables (IVs) are associated with blood pressure. (ii) the genetic variants are not associated with any confounders of the exposure-outcome relationship. (iii) the genetic variants are associated with the outcome only through change in BP *i.e.* a lack of pleiotropy.

The inverse-variance weighted (IVW) method with a multiplicative random-effect model[69], MR-Egger and MR-PRESSO were used. We also performed several sensitivity analyses to assess the robustness of our results to potential violations of the Mendelian Randomisation assumptions given these analyses have different assumptions for validity. To assess instrument strength, we computed the F statistic[70] for the association of genetic variants with SBP, DBP and PP, respectively. MR-Egger regression generates valid estimates even if not all the genetic instruments are valid, as long as the InSIDE (Instrument Strength Independent of Direct Effect) assumption holds[71] and also test if there is unbalanced pleiotropy. MR-PRESSO permits removal of outlier IVs[72]. To minimise pleiotropy, we removed SNVs associated with cardiovascular traits, including cholesterol level (LDL/HDL/triglycerides), smoking, Type 2 diabetes (T2D) and Atrial Fibrillation (AF) (Supplementary Table 22c). Although these methods may have different statistical power, the rationale is that if these methods give a similar conclusion regarding the association of BP and CVD, then we are more confident in inferring that the positive results are unlikely driven by violation of the MR assumptions[73].

We performed a genetic analysis of BP plus BP trait specific analyses of SBP, DBP, PP (online methods) using both previously published and newly identified BP SNVs. We considered any stroke, any ischemic stroke, large artery stroke, cardioembolic stroke, small vessel stroke and coronary artery disease (CAD) (online methods). As expected, blood pressure was positively associated with increased stroke (any stroke) risk (odds ratio (95% confidence interval) = 1.42 (1.36 - 1.49) per increase of one standard deviation in inverse-normal transformed of generic blood pressure (BPgeneric), $P = 5.70 \times 10^{-50}$; 1.71 (1.61 - 1.82) per increase of one standard deviation of inverse-normal transformed of SBP, $P = 1.35 \times 10^{-67}$; 1.53 (1.44 - 1.64) per increase of one standard deviation in inverse-normal transformed of DBP, $P = 2.34 \times 10^{-37}$; 1.39 (1.31 - 1.47) per increase of one standard deviation of inverse-normal transformed of PP, $P = 3.62 \times 10^{-28}$). MR-EGGER and MR-PRESSO gave similar results (Supplementary Table 22) and no significant pleiotropy was detected ($P>0.01$ for the MR-EGGER intercept; Supplementary Table 22). The positive association with stroke subtypes were statistically significant ($P<0.00069$; Figure 4, Supplementary Table 22), with the largest effect size of blood pressure on large artery stroke while smallest effect was with cardioembolic stroke. SBP was the primary association - with the largest effect size, with any of the CVD traits investigated (Figure 4, Supplementary Table 22), suggesting that SBP is the most sensitive BP measure, consistent with clinical practice.

In MR-Egger, we tested if the intercept estimate deviated from zero for the inference of genetic pleiotropy, i.e. where certain genetic variants affect the outcome through a different biological pathway from BP. In practice, there was little evidence that the MR-Egger intercept deviated from zero for any BP traits and any CVD traits, e.g. SBP and large artery stroke (intercept = 0.0026, SE = 0.0025, $P = 0.31$).

With MR-PRESSO, we used the outlier test embedded in the R package 'MR-PRESSO' to remove outlier due to pleiotropy and estimated the causal effects by IVW method before and after outlier removal. The causal effects (OR) after outlier-corrected were similar to the 'raw' estimates

(Supplementary Table 22: with MR-PRESSO results), indicating that there was little evidence for genetic pleiotropy.

To quantify the strength of the selected instrumental variants for each "exposure (BP) – outcome (CVD)" pairs, we computed *F*-statistics (Supplementary Table 22). The *F*-statistics for the 964 SNVs for the "BP generic – Any Stroke" ranged from 11 to 767 with a median of 44, well above the threshold of $F > 10$ typically recommended for MR analysis [74].

When performing a multi-variable MR analyses including both SBP and DBP in the model for the inference of their effects on stroke, we found that the effect of SBP is still significant after adjusting for DBP, but not vice versa. Interestingly, we found that the effect of SBP on large artery stroke (P=7.21 × 10^{-23}; OR(95%CI)=2.62 (2.16, 3.17)per increase of one standard deviation of inverse-normal transformed of SBP) after adjusting for DBP is larger than the univariate MR estimation (P=1.30 × 10^{-33}; 2.19 (1.93, 2.48)), while the effect of DBP becomes negatively associated with stroke risk (P=6.28 × 10^{-2}; 0.832 (0.686, 1.01)) adjusting for SBP (although this did not pass our *P*-value threshold for significance). This is consistent with the findings from the univariable MR analysis of PP on stroke risk, which showed that PP has the largest effect on large artery stroke.

We also performed sensitivity analysis using multivariable MR-Egger to correct for pleiotropy[75]. Similar to the univariable MR-Egger results, there was little evidence that the multi-variable MR-Egger intercept deviated from zero for any BP traits and any CVD outcomes ($P_{\text{intercept}} > 0.01$).

Variance explained by BP-associated SNVs

We used 5,390 individuals from the Danish cohort within EPIC-CVD[76] to calculate variance explained as these participants were not used as part of the discovery set, genotyped using the Illumina Human CoreExome BeadChip array. SBP and DBP were measured twice at baseline and the average was used. Using a genetic risk score to represent all the known and new BP associations, we fitted a linear regression of each transformed BP trait against age, age^2, sex, BMI, top 10 genetic principle components, and CVD event (defined as any first CVD event) as a factor to obtained the variance explained by covariates ($R^2_{covariants}$). We then fit a second linear model for the transformed BP trait with all covariates plus a GRS to obtain the variance explained by all variables (R^2_{all}). Thus, the variance explained by GRS of BP genetic variants was:

$R^2_{GRS} = R^2_{all} - R^2_{covariants}$

We considered five different levels of GRS for each BP trait: (i) all independent common variants (MAF >= 0.01); (ii) all independent rare variants (MAF < 0.01); (iii) all independent SNVs within known loci; (iv) all independent SNVs within novel loci; (v) all independent SNVs.

The estimated percentage of variance in BP explained by all the BP-associated SNVs (known and novel) was: 4.54 for SBP, 3.54 for DBP, and 5.39 for PP (Supplementary Table 26). This is consistent with previous reports. Within the novel loci, ~0.6% of the variance is explained by the new independent SNVs, with <0.2% of the variance explained by independent rare variants (although we note only ~ 50% of rare variants were available for this calculation).

Supplementary Table 26:
Percentage of variance explained for BP traits in the EPIC-CVD Danish cohort.

BP trait	Number of SNPs for constructing the GRS				
	ALL	COMM	RARE	KNOWN	NOVEL
SBP	778	734	44	507	271
DBP	742	708	34	494	248
PP	802	760	42	569	233

BP trait	% variance explained by GRS				
	ALL	COMM	RARE	KNOWN	NOVEL
SBP	4.54	4.55	0.17	4.54	0.62
DBP	3.541	3.421	0.183	3.311	0.601
PP	5.39	5.4	0.05	5.09	0.59

ALL = GRS of all associated variants for any BP trait
COMM = GRS of all common and low-frequency variants (MAF >= 0.01)
RARE = GRS of all rare variants (MAF < 0.01)
KNOWN = GRS of all known variants
NOVEL = GRS of novel variants identified in current study

UK Biobank specific analyses

The UK Biobank (UKBB) is a large prospective study of 502,642 participants aged 40–69 years when recruited between 2006–2010 at 22 assessment centres across the United Kingdom[77,78]. The study has collected and continues to collect a large amount of phenotypic measurements including systolic and diastolic blood pressure (BP).

Processing, quality control and analyses of the data provided by UK Biobank, were performed at two sites independently and were confirmed to be concordant at each step of the process.

Blood pressure measurement

BP was measured twice in a seated position after two minutes rest with a one minute rest before the second measurement [UK Biobank. UKB : Resource 100225 - Blood-pressure measurement procedures using ACE - Version 1.0. Available at: http://biobank.ctsu.ox.ac.uk/crystal/refer.cgi?id=100225. Accessed October 2, 2017]. An appropriate cuff and an Omron 705IT digital BP monitor, was used to measure BP in the majority of participants (UK Biobank data fields: SBP: f.4080.0.0 and f.4080.0.1; DBP: f.4079.0.0 and f.4079.0.1). If the largest cuff size was too small for the participant, or the electronic BP monitor failed, a sphygmomanometer with an inflatable cuff was used in conjunction with a stethoscope to perform a manual measurement (UK Biobank data fields: SBP: f.93.0.0 and f.93.0.1; DBP: f.93.0.0 and f.93.0.1). Of the 502,642 UKBB participants, 488,366 had both BP measurements and genotype data available, we therefore restricted phenotype quality control (QC) to these individuals. At baseline there were 446,611 participants with two automated BP measurements; 14,133 participants with one automated and one manual measurement and 26,615 with both manual measurements. The 1,007 samples with only one blood pressure measurement at baseline were excluded. Comparison of the BP distributions obtained using automated and manual approaches were concordant and reassured us both approaches were accurate. Individuals missing SBP or DBP at baseline assessment were removed (n=1,834). The mean of both measurements at baseline for a given participant was calculated to create an overall measure for SBP, DBP and PP. Phenotype QC was performed in R version v3.3.

Blood pressure measurement quality control Participants were excluded from analysis if

1. the difference between the first and second blood pressure measurement > 99.9th percentile (n=857);
2. covariates were missing: Age (n=0), gender (n=0), BMI (n=3105) using respectively UK Biobank data fields: f.21003.0.0, f.31.0.0 and f.21001.0.0;
3. they were pregnant at time of blood pressure measurement (n=131) UK Biobank data field: f.3140.0.0;
4. BMI >99.9th or <0.01 percentile (n=970).

In total 483,515 participants remained following quality control.

Adjustment of BP measurement for treatment effect For all UKBB participants that were on anti-hypertensive medication at time of blood pressure measurement (n=48,800) we added 15mmHg to the mean observed SBP, 10mmHg to the mean observed DBP and 5mmHg to the mean observed PP.

Definition of hypertension UKBB participants were defined as having hypertension when at least one of the following criteria was met:

1. Mean observed SBP ≥ 140 mmHg
2. Mean observed DBP ≥ 90 mmHg
3. History of hypertension: which was defined using the "non-cancer illnesses and associated first diagnosis timestamp" collected through the verbal interview (UK Biobank data field: f.20002.0.0) at baseline assessment for each UKBB participant. That is, where the following codes: "1065 hypertension", "1072 essential hypertension" are present in data field f.20002.0.0. No ICD codes were used to define hypertension.
4. Use of anti-hypertensive medication: at a baseline survey, we used responses to the "Medication for cholesterol, blood pressure or diabetes" question for males and responses to the "Medication for cholesterol, blood pressure, diabetes, or take exogenous hormones" question for females, both collected through the touchscreen questionnaire and providing information on regular medication use (UK Biobank data fields: f.6177.0.0 and f.6153.0.0, respectively). If a participant selected "2 Blood pressure medication" we defined this participant as having a current status of taking anti-hypertensive medication (27,931 females, 22,630 males).

255,794 individuals were defined as hypertensive and 227,721 were non-hypertensive.

Genotype quality control (Supplementary Figure 5)

We used both the Affymetrix UK Biobank/BiLEVE array genotypes and the Human Reference Consortium imputed genotypes[78]. Genotype QC was performed using PLINK1.9 and R v3.3.

Defining a European set of UK Biobank participants Approximately 22,000 UKBB participants had a self-reported ethnic background outside of Europe[78]. Deviation from Hardy Weinberg Equilibrium (HWE) is often an indicator of a poorly genotyped variant. However, due to the ethnic diversity of the UKBB cohort, deviations from HWE could also be due to violation of the assumptions of HWE *e.g.* large differences in allele frequency in an ethnically mixed cohort. We therefore sought to define a genetically European group of UKBB participants using principal component analyses (PCA) with FlashPCA2[79]. High-quality autosomal variants were selected for PCA based on an overall call rate ≥99%; minor allele frequency (MAF) >=0.05 and HWE $P \geq 10^{-5}$. Regions of the genome known to exhibit long-range linkage disequilibrium (LD) were removed (chr6:25–33.5 Mb, chr8:8–12 Mb, chr17:40.4–42.4 Mb) to ensure the PCs were picking up ancestry and not LD. These variants were then LD pruned so no pair of variants within a 100 variant window had $R^2>0.2$. A final round of LD pruning was performed in a 1000 variant window.

Having generated 50 PCs, we adopted the method of Astle et al.[80], to identify ancestral outliers to be remove. In brief, a 'genetic distance',

$$d(i) = \sqrt{\sum_{m=1}^{15} E_m (P_{im} - C_m)^2}$$

, between individual *i* and a hypothetical median ''white British'' participant was calculated, where E_m represents the eigenvalue corresponding to PC, m (*i.e.* the genetic

variance explained by PC_m), P_{im} represents the score of individual i on PC_m, C_m represents the median score on PC_m of participants with self-reported White ancestry (defined as "British", "Irish", "White" or "Any other White background").
We used a threshold of genetic distance > 0.2 to identify non-Europeans, which resulted in the exclusion of 23,511 non-European participants.

Batch level variant and sample QC Genotype QC was performed with the above defined European subset of participants, separately for each of the 106 UKBB genotyping batches. The following thresholds were applied to remove variants: call rate ≤ mean (call rate) - [3 x SD (call rate)]; HWE *P*-value < $1x10^{-12}$ (MAF<0.01) or HWE *P*-value < $1x10^{-6}$ (MAF≥0.01). Variants that failed either call rate or HWE within a batch were excluded from the corresponding batch prior to batch-level sample QC. Within batch, samples with call rate < mean (call rate) - [3 x SD (call rate)] or Heterozygosity > (mean +/- 3SD) were removed (n=11,944).

Variant and sample QC across all batches Variants that failed QC in >48 batches (UKBB array) or > 3 batches (UK BiLEVE array) were excluded (n=23,221 SNVs). We excluded samples who's genetic sex and phenotypically defined sex (as provided by the UKBB) were discordant (n=136 samples).
After variant and sample QC across all batches we performed a second PCA with FlashPCA2[79] using the same approach to select variants for PCA as described above. A genetic distance measure of 0.175 calculated using 8PCs (as described above) was used to remove a further 3,015 individuals of non-European ancestry.

Definition of an unrelated set of UK Biobank participants For analyses of hypertension, we chose not to use a mixed effects model due to limitations with calculating a full kinship matrix. Therefore, using the fully QC'd data, we defined a subset of unrelated UKBB participants using the kinship information provided by UKBB that lists the kinship coefficient of pairs of individuals up to 3rd degree relatives. We calculated sample call rate to guide which participant within a pair of relatives to remove. All pairs that shared individual(s) were aggregated into families. From each of these families the sample with the highest call rate was retained. If individuals within the family had the same call rate we chose the one that occurred first in the file.

Imputation The pre-imputation variant QC, phasing and imputation performed on the combined UKBB and UK BiLEVE data has been described in detail elsewhere[78]. The genetic data were imputed using the Haplotype Reference Consortium (HRC) panel. Additional variants were available in the interim release of imputed using 1000G/UK10K data in 150,000 UKBB participants but were not part of the HRC imputation panel. We extracted 30,315 variants that were readily available in the first release UKBB imputation dataset and were genotyped on the exome array but not either of the Affymetrix arrays used by UKBB. After QC of these variants and using an information score threshold >0.3, 157,666 variants were available for analysis in ~150,000 participants from the interim release.
Variants for which both genotype and imputation data were available, we used the imputed variant if the genotyping call rate was <0.98 and the variant was imputed with an information score >0.7. We used the genotyped data for all variants that did not satisfy these criteria. All variants that passed QC and were available in either the genotyped or imputed data alone were also analysed.

In total, 39,312,035 imputed variants with info>0.3 of which 31,835,351 were low frequency or rare were analysed in GWAS of UKBB (175,430 were Exome array variants of which 59,824 variants were genotyped and 115,606 variants were imputed). A further 784055 genotyped variants were analysed of which 405,033 were rare or low-frequency. Of these, up to 175,430 variants were analysed in EAWAS (Stage 1), and up to 29,454,346 additional variants – in RV-GWAS (Stage 1)

Final dataset used for exome content analyses Following QC, 156,481 variants from the UK-Biobank full release (were analysed in 445,360 participants of European ancestry) and 18,947 variants from the interim release were analyzed in 364,510 European participants with SBP, DBP and PP measurements. Following QC and transformation, 157,666 Exome array variants (62,032 genotyped and 95,634 imputed) were tested for association with HTN in up to 364,565 unrelated European participants.

Analyses of SBP DBP and PP

Each of the continuous traits (SBP, DBP and PP) were regressed on baseline age, baseline age squared, gender, BMI and genotyping array using the lm function in R. The residuals from these regression models were rank transformed and inverse normalised and the resulting transformed SBP, DBP and PP residuals were analysed using linear mixed models implemented in BOLT-LMM (Version: v2.3). The set of QCd variants used for the second PCA were also used for BOLT-LMM model building.

In total, 784,045 directly genotyped and 39,312,035 imputed variants (175,430 were Exome array variants of which 59,824 variants were genotyped and 115,606 variants were imputed) were analysed for association with SBP, DBP and PP in up to 445,415 individuals of European ancestry from UKBB.

Analyses of hypertension

Genetic analysis of exome array variants was performed for hypertension as a binary outcome in 364,510 unrelated individuals (192,235 hypertensive cases and 172,275 controls) of European ancestry using SNPTEST (Version: v2.5.4-beta3). Analyses were adjusted for baseline age, baseline age squared, gender, BMI, genotyping array and the first eight ancestry principal components (PCs).

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INTERVAL (Metabolite measurement using Metabolon HD4 platform)

Participants in the INTERVAL randomised controlled trial were recruited with the active collaboration of NHS Blood and Transplant England (www.nhsbt.nhs.uk), which has supported field work and other elements of the trial. DNA extraction and genotyping was co-funded by the National Institute for Health Research (NIHR), the NIHR BioResource (http://bioresource.nihr.ac.uk/) and the NIHR [Cambridge Biomedical Research Centre at the Cambridge University Hospitals NHS Foundation Trust] [*].The academic coordinating centre for INTERVAL was supported by core funding from: NIHR Blood and Transplant Research Unit in Donor Health and Genomics (NIHR BTRU-2014-10024), UK Medical Research Council (MR/L003120/1), British Heart Foundation (SP/09/002; RG/13/13/30194; RG/18/13/33946) and the NIHR [Cambridge Biomedical Research Centre at the Cambridge University Hospitals NHS Foundation Trust] [*]. A complete list of the investigators and contributors to the INTERVAL trial is provided in reference [**]. The academic coordinating centre would like to thank blood donor centre staff and blood donors for participating in the INTERVAL trial.

This work was supported by Health Data Research UK, which is funded by the UK Medical Research Council, Engineering and Physical Sciences Research Council, Economic and Social Research Council, Department of Health and Social Care (England), Chief Scientist Office of the Scottish Government Health and Social Care Directorates, Health and Social Care Research and Development Division (Welsh Government), Public Health Agency (Northern Ireland), British Heart Foundation and Wellcome.

*The views expressed are those of the authors and not necessarily those of the NHS, the NIHR or the Department of Health and Social Care.

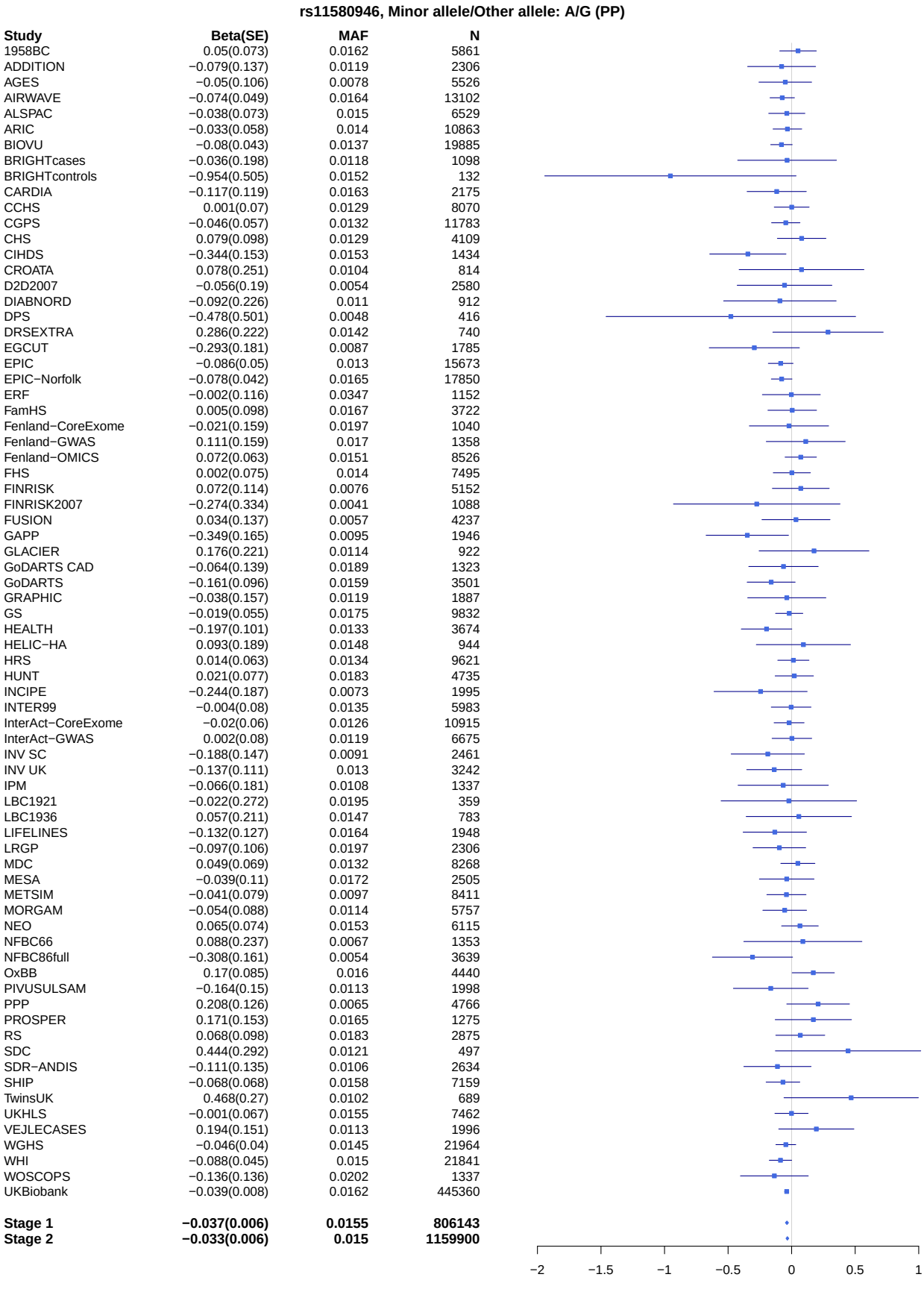
**Di Angelantonio E, Thompson SG, Kaptoge SK, Moore C, Walker M, Armitage J, Ouwehand WH, Roberts DJ, Danesh J, INTERVAL Trial Group. Efficiency and safety of varying the frequency of whole blood donation (INTERVAL): a randomised trial of 45 000 donors. Lancet. 2017 Nov 25;390(10110):2360-2371.

EPIC Norfolk (Metabolite measurement using Metabolon HD4 platform)

The EPIC-Norfolk study (https://doi.org/10.22025/2019.10.105.00004) has received funding from the Medical Research Council (MR/N003284/1 and MC-UU_12015/1) and Cancer Research UK (C864/A14136). The genetics work in the EPIC-Norfolk study was funded by the Medical Research Council (MC_PC_13048). Metabolite measurements in the EPIC-Norfolk study were supported by the MRC Cambridge Initiative in Metabolic Science (MR/L00002/1) and the Innovative Medicines Initiative Joint Undertaking under EMIF grant agreement no. 115372. We are grateful to all the participants who have been part of the project and to the many members of the study teams at the University of Cambridge who have enabled this research.

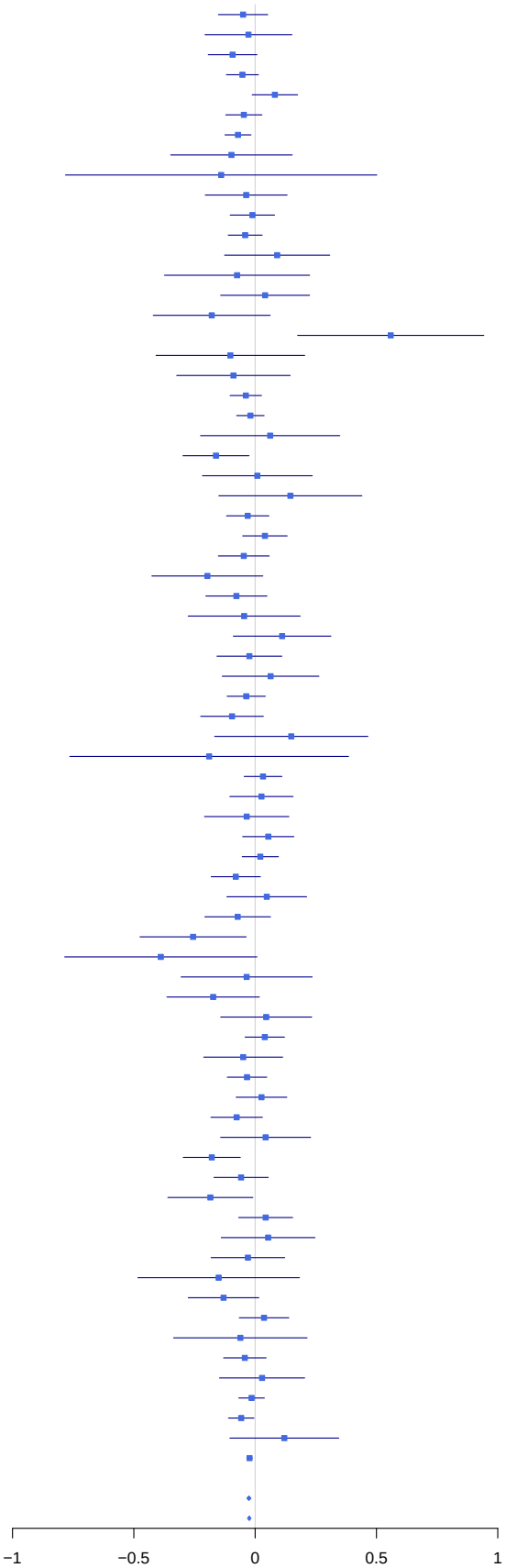
Supplementary Figures

Supplementary Figure 1. Forest plots for unique rare SNVs associated with one or more BP traits.



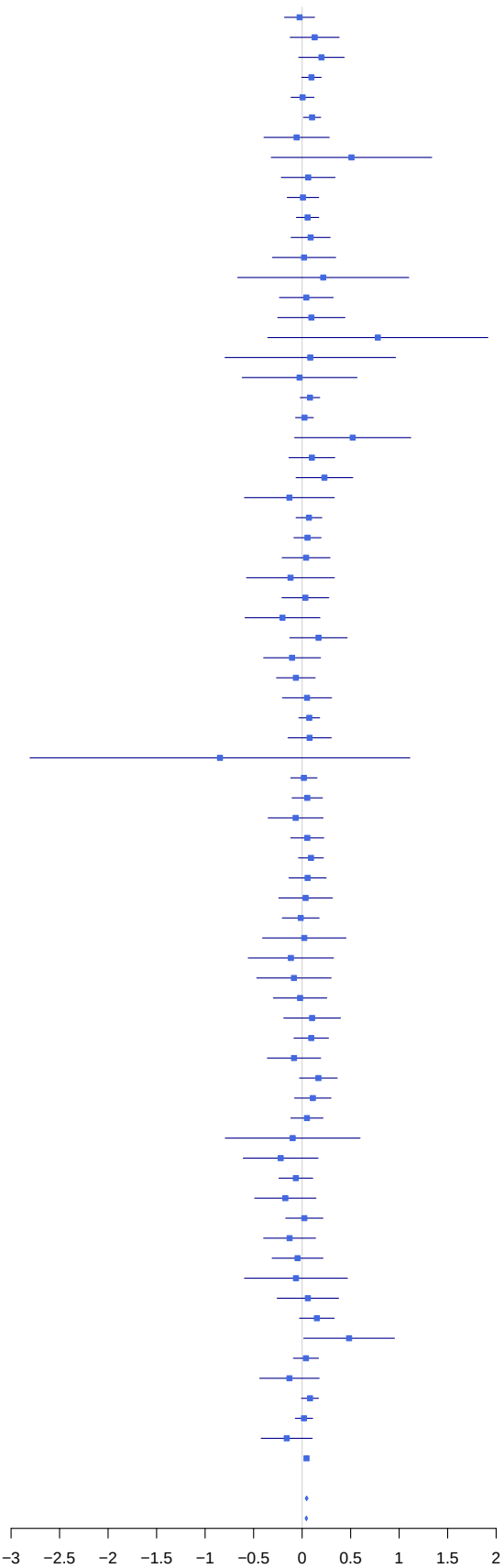
rs11699758, Minor allele/Other allele: T/C (PP)

Study	Beta(SE)	MAF	N
1958BC	−0.05(0.052)	0.0328	5861
ADDITION	−0.028(0.091)	0.026	2306
AGES	−0.093(0.051)	0.0366	5526
AIRWAVE	−0.052(0.034)	0.0354	13102
ALSPAC	0.081(0.048)	0.0359	6529
ARIC	−0.047(0.038)	0.0326	10863
BIOVU	−0.071(0.027)	0.035	19885
BRIGHTcases	−0.098(0.128)	0.0296	1098
BRIGHTcontrols	−0.14(0.327)	0.0379	132
CARDIA	−0.037(0.086)	0.0323	2175
CCHS	−0.011(0.047)	0.0291	8070
CGPS	−0.041(0.036)	0.0336	11783
CIHDS	0.091(0.111)	0.0303	1434
CROATA	−0.075(0.153)	0.0258	814
D2D2007	0.041(0.094)	0.0236	2580
DIABNORD	−0.179(0.123)	0.0367	912
DPS	0.559(0.196)	0.0337	416
DRSEXTRA	−0.102(0.156)	0.0264	740
EGCUT	−0.089(0.119)	0.0199	1785
EPIC	−0.038(0.033)	0.0301	15673
EPIC−Norfolk	−0.02(0.029)	0.0352	17850
ERF	0.062(0.146)	0.0222	1152
FamHS	−0.161(0.07)	0.0315	3722
Fenland−CoreExome	0.009(0.115)	0.038	1040
Fenland−GWAS	0.145(0.15)	0.0273	1358
Fenland−OMICS	−0.031(0.045)	0.0304	8526
FHS	0.04(0.047)	0.0352	7495
FINRISK	−0.047(0.053)	0.0354	5152
FINRISK2007	−0.197(0.117)	0.0354	1088
FUSION	−0.077(0.064)	0.0295	4237
GLACIER	−0.045(0.118)	0.0401	922
GoDARTS CAD	0.111(0.103)	0.037	1323
GoDARTS	−0.024(0.068)	0.0318	3501
GRAPHIC	0.064(0.102)	0.0297	1887
GS	−0.037(0.04)	0.0328	9832
HEALTH	−0.095(0.066)	0.0321	3674
HELIC−HA	0.149(0.161)	0.0222	944
HELIC−HP	−0.19(0.293)	0.0106	565
HRS	0.032(0.04)	0.034	9621
HUNT	0.026(0.066)	0.0247	4735
INCIPE	−0.035(0.089)	0.0319	1995
INTER99	0.054(0.054)	0.0304	5983
InterAct−CoreExome	0.021(0.038)	0.0328	10915
InterAct−GWAS	−0.08(0.052)	0.0299	6675
INV SC	0.048(0.084)	0.0289	2461
INV UK	−0.072(0.069)	0.0341	3242
IPM	−0.256(0.112)	0.0303	1337
LBC1921	−0.389(0.202)	0.0334	359
LBC1936	−0.035(0.138)	0.0332	783
LIFELINES	−0.173(0.097)	0.0277	1948
LRGP	0.046(0.096)	0.0249	2306
MDC	0.04(0.041)	0.037	8268
MESA	−0.049(0.083)	0.0303	2505
METSIM	−0.033(0.042)	0.0389	8411
MORGAM	0.026(0.053)	0.0317	5757
NEO	−0.076(0.054)	0.0288	6115
NFBC66	0.043(0.095)	0.0418	1353
NFBC86full	−0.179(0.06)	0.0398	3639
OxBB	−0.058(0.057)	0.0357	4440
PIVUSULSAM	−0.185(0.089)	0.0318	1998
PPP	0.043(0.057)	0.033	4766
PROSPER	0.054(0.099)	0.0424	1275
RS	−0.03(0.077)	0.0298	2875
SDC	−0.15(0.17)	0.0352	497
SDR−ANDIS	−0.13(0.074)	0.0366	2634
SHIP	0.037(0.052)	0.0268	7159
TwinsUK	−0.061(0.14)	0.0399	689
UKHLS	−0.043(0.045)	0.0344	7462
VEJLECASES	0.028(0.09)	0.0326	1996
WGHS	−0.015(0.027)	0.0327	21964
WHI	−0.057(0.027)	0.0327	21841
WOSCOPS	0.12(0.114)	0.0295	1337
UKBiobank	−0.023(0.006)	0.0345	445360
Stage 1	**−0.026(0.004)**	**0.0339**	**800653**
Stage 2	**−0.024(0.004)**	**0.0339**	**1154410**



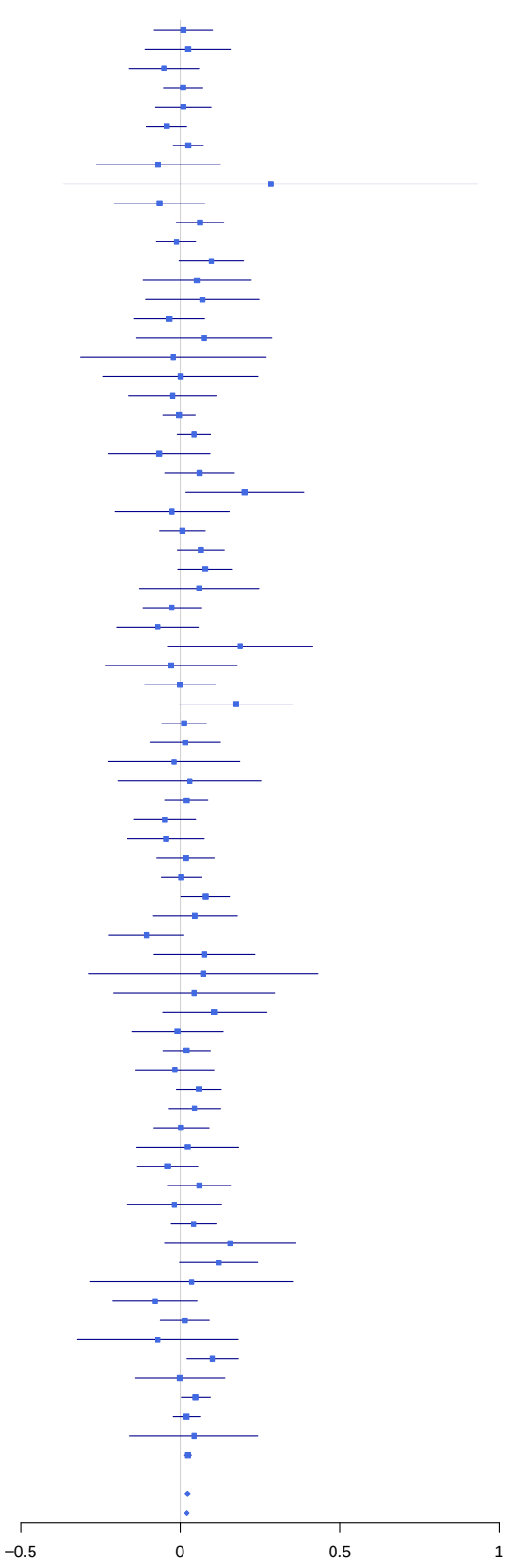
rs117874826, Minor allele/Other allele: C/A (SBP)

Study	Beta(SE)	MAF	N
1958BC	−0.026(0.079)	0.0141	5864
ADDITION	0.129(0.129)	0.0134	2307
AGES	0.199(0.12)	0.0064	5526
AIRWAVE	0.096(0.051)	0.015	13102
ARIC	0.005(0.06)	0.0127	10864
BIOVU	0.102(0.045)	0.0123	19885
BRIGHTcases	−0.057(0.172)	0.0159	1098
BRIGHTcontrols	0.509(0.422)	0.0227	132
CARDIA	0.063(0.142)	0.0117	2175
CCHS	0.009(0.083)	0.009	8070
CGPS	0.057(0.059)	0.0122	11784
CHS	0.088(0.103)	0.0113	4113
CIHDS	0.02(0.166)	0.0129	1436
CROATA−KORCULA	0.218(0.45)	0.0031	814
D2D2007	0.044(0.141)	0.0095	2580
DIABNORD	0.095(0.177)	0.017	912
DPS	0.78(0.579)	0.0036	416
DRSEXTRA	0.084(0.448)	0.0034	740
EGCUT	−0.026(0.302)	0.0031	1785
EPIC	0.081(0.051)	0.0122	15676
EPIC−Norfolk	0.024(0.047)	0.013	17850
ERF	0.521(0.306)	0.0048	1153
FamHS	0.1(0.121)	0.0108	3722
Fenland−CoreExome	0.23(0.149)	0.0226	1040
Fenland−GWAS	−0.131(0.236)	0.0154	1358
Fenland−OMICS	0.07(0.068)	0.0127	8526
FHS	0.055(0.071)	0.0149	7495
FINRISK	0.041(0.126)	0.0062	5152
FINRISK2007	−0.12(0.231)	0.0087	1088
FUSION	0.034(0.123)	0.0079	4237
GAPP	−0.203(0.197)	0.0062	1947
GLACIER	0.169(0.151)	0.0239	922
GoDARTS CAD	−0.104(0.15)	0.0174	1323
GoDARTS	−0.064(0.102)	0.0139	3501
GRAPHIC	0.051(0.129)	0.0175	1887
GS	0.074(0.055)	0.0177	9832
HEALTH	0.077(0.114)	0.0105	3674
HELIC−HP	−0.847(0.999)	9e−04	565
HRS	0.018(0.069)	0.0111	9621
HUNT	0.053(0.08)	0.0169	4735
INCIPE	−0.067(0.145)	0.0123	1995
INTER99	0.053(0.087)	0.0114	5986
InterAct−CoreExome	0.092(0.065)	0.0109	10915
InterAct−GWAS	0.056(0.098)	0.011	6675
INV SC	0.036(0.141)	0.01	2461
INV UK	−0.014(0.097)	0.0163	3242
IPM	0.022(0.22)	0.0071	1337
LBC1921	−0.116(0.224)	0.0292	359
LBC1936	−0.084(0.196)	0.0172	783
LIFELINES	−0.021(0.14)	0.0133	1948
LRGP	0.103(0.149)	0.01	2306
MDC	0.094(0.091)	0.0074	8268
MESA	−0.083(0.14)	0.0104	2505
METSIM	0.168(0.099)	0.0061	8411
MORGAM	0.11(0.096)	0.0095	5757
NEO	0.05(0.085)	0.0114	6117
NFBC66	−0.097(0.354)	0.003	1353
NFBC86full	−0.221(0.197)	0.0036	3639
OxBB	−0.065(0.089)	0.0144	4440
PIVUSULSAM	−0.173(0.161)	0.0098	1998
PPP	0.023(0.098)	0.0111	4766
PROSPER	−0.129(0.137)	0.022	1275
RS	−0.047(0.134)	0.0096	2875
SDC	−0.063(0.271)	0.0141	498
SDR−ANDIS	0.059(0.161)	0.0074	2636
SHIP	0.152(0.091)	0.0084	7161
TwinsUK	0.484(0.239)	0.0131	689
UKHLS	0.039(0.066)	0.0155	7462
VEJLECASES	−0.131(0.156)	0.0105	1996
WGHS	0.081(0.045)	0.0117	21964
WHI	0.019(0.046)	0.011	21841
WOSCOPS	−0.159(0.134)	0.0209	1337
UKBiobank	0.045(0.01)	0.0147	445360
Stage 1	**0.047(0.007)**	**0.0138**	**799262**
Stage 2	**0.044(0.006)**	**0.0132**	**1153360**



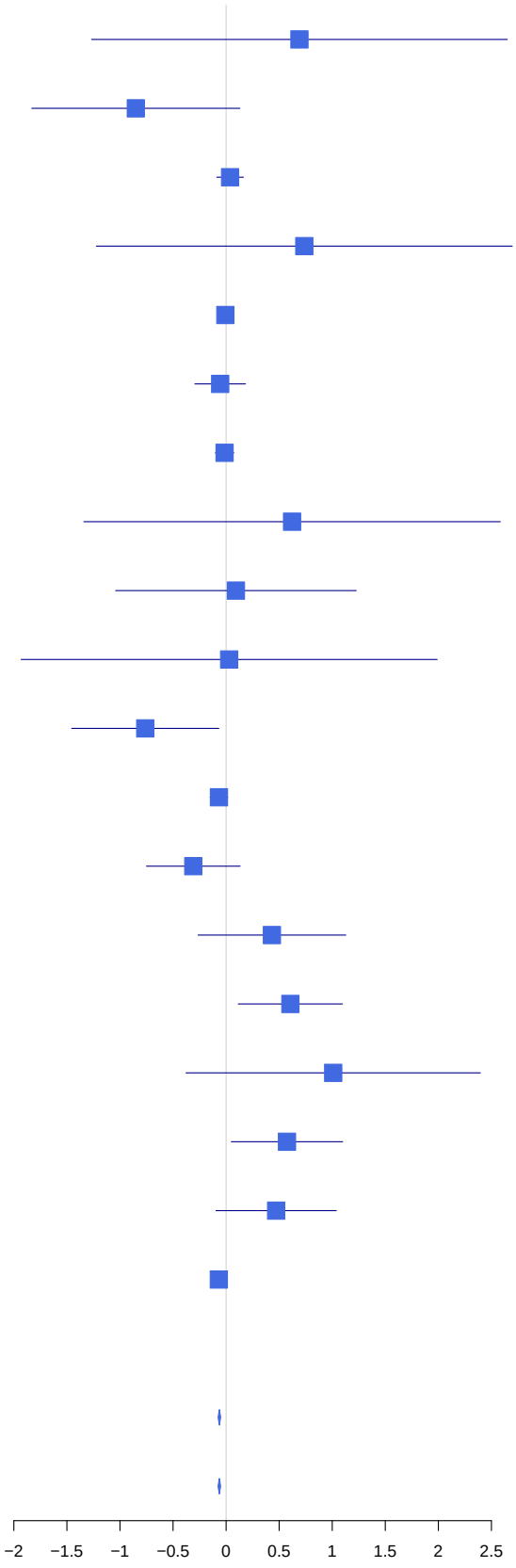
rs11937432, Minor allele/Other allele: G/A (DBP)

Study	Beta(SE)	MAF	N
1958BC	0.009(0.048)	0.0396	5864
ADDITION	0.024(0.069)	0.0453	2307
AGES	−0.051(0.056)	0.032	5526
AIRWAVE	0.009(0.032)	0.0421	13102
ALSPAC	0.009(0.045)	0.0404	6529
ARIC	−0.043(0.032)	0.0492	10863
BIOVU	0.024(0.024)	0.0446	19885
BRIGHTcases	−0.07(0.099)	0.0501	1098
BRIGHTcontrols	0.284(0.332)	0.0379	132
CARDIA	−0.065(0.073)	0.0458	2175
CCHS	0.062(0.038)	0.0463	8070
CGPS	−0.013(0.032)	0.0454	11783
CHS	0.098(0.052)	0.0481	4109
CIHDS	0.052(0.087)	0.0492	1434
CROATA−KORCULA	0.069(0.091)	0.0812	814
D2D2007	−0.035(0.057)	0.0672	2580
DIABNORD	0.074(0.109)	0.0515	912
DPS	−0.022(0.148)	0.0565	416
DRSEXTRA	0.001(0.124)	0.0466	740
EGCUT	−0.024(0.07)	0.0625	1785
EPIC	−0.004(0.026)	0.0491	15674
EPIC−Norfolk	0.043(0.026)	0.0419	17850
ERF	−0.066(0.081)	0.0824	1153
FamHS	0.061(0.055)	0.0539	3722
Fenland−CoreExome	0.202(0.094)	0.0529	1040
Fenland−GWAS	−0.026(0.091)	0.0478	1358
Fenland−OMICS	0.007(0.036)	0.0464	8526
FHS	0.065(0.038)	0.0586	7495
FINRISK	0.078(0.043)	0.0557	5153
FINRISK2007	0.06(0.096)	0.0551	1088
FUSION	−0.026(0.047)	0.0583	4237
GAPP	−0.072(0.066)	0.0655	1946
GLACIER	0.187(0.115)	0.0434	922
GoDARTS CAD	−0.029(0.105)	0.0351	1323
GoDARTS	−0.001(0.057)	0.047	3501
GRAPHIC	0.175(0.09)	0.0368	1887
GS	0.012(0.036)	0.0439	9832
HEALTH	0.015(0.056)	0.0462	3674
HELIC−HA	−0.02(0.106)	0.0508	944
HELIC−HP	0.03(0.114)	0.0681	565
HRS	0.019(0.034)	0.0471	9621
HUNT	−0.048(0.05)	0.0452	4735
INCIPE	−0.045(0.061)	0.072	1995
INTER99	0.017(0.046)	0.042	5984
InterAct−CoreExome	0.003(0.032)	0.0474	10915
InterAct−GWAS	0.079(0.039)	0.0513	6675
INV SC	0.046(0.067)	0.048	2461
INV UK	−0.106(0.06)	0.0453	3242
IPM	0.075(0.081)	0.0626	1342
LBC1921	0.072(0.184)	0.0418	359
LBC1936	0.043(0.129)	0.0421	783
LIFELINES	0.107(0.083)	0.0393	1948
LRGP	−0.008(0.073)	0.0434	2306
MDC	0.019(0.038)	0.046	8268
MESA	−0.017(0.064)	0.0513	2505
METSIM	0.059(0.036)	0.0521	8411
MORGAM	0.044(0.041)	0.0556	5757
NEO	0.002(0.044)	0.0443	6115
NFBC66	0.023(0.081)	0.0606	1353
NFBC86full	−0.039(0.048)	0.064	3639
OxBB	0.06(0.051)	0.0453	4440
PIVUSULSAM	−0.019(0.076)	0.0458	1998
PPP	0.042(0.037)	0.0923	4766
PROSPER	0.156(0.104)	0.0384	1275
RS	0.121(0.063)	0.0452	2875
SDC	0.036(0.162)	0.0371	498
SDR−ANDIS	−0.079(0.068)	0.0444	2636
SHIP	0.014(0.039)	0.0483	7160
TwinsUK	−0.072(0.129)	0.045	689
UKHLS	0.1(0.041)	0.0421	7462
VEJLECASES	−0.001(0.072)	0.0516	2002
WGHS	0.048(0.023)	0.0482	21964
WHI	0.019(0.022)	0.051	21841
WOSCOPS	0.043(0.103)	0.0374	1337
UKBiobank	0.023(0.005)	0.0426	445360
Stage 1	**0.022(0.004)**	**0.0457**	**806731**
Stage 2	**0.02(0.003)**	**0.046**	**1160520**



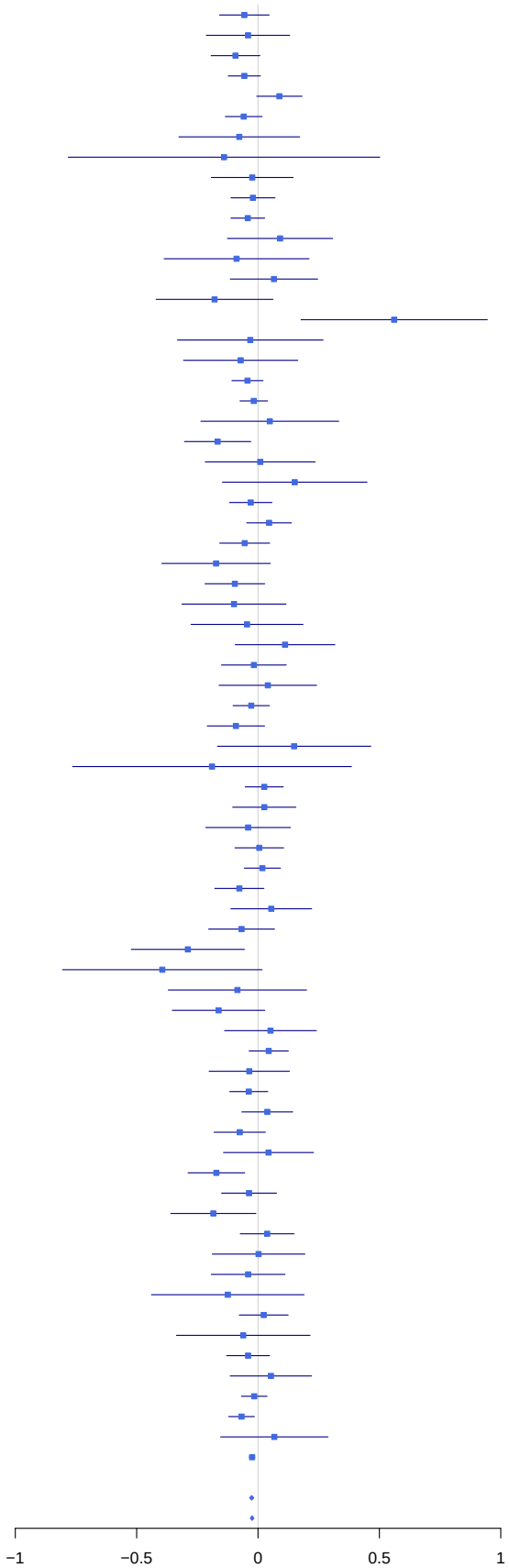
rs1229984, Minor allele/Other allele: T/C (PP)

Study	Beta(SE)	MAF	N
1958BC	0.691(0.999)	1e−04	5861
ADDITION	−0.851(0.5)	9e−04	2306
ALSPAC	0.038(0.064)	0.0198	6529
BRIGHTcases	0.737(1)	5e−04	1098
EPIC−Norfolk	−0.007(0.031)	0.0296	17850
Fenland−GWAS	−0.056(0.122)	0.0293	1358
Fenland−OMICS	−0.014(0.044)	0.0314	8526
GoDARTS CAD	0.622(1.001)	4e−04	1323
HEALTH	0.093(0.578)	4e−04	3674
HUNT	0.029(1)	1e−04	4735
INTER99	−0.762(0.354)	7e−04	5983
InterAct−GWAS	−0.067(0.042)	0.0459	6675
IPM	−0.309(0.225)	0.0077	1337
MDC	0.432(0.355)	5e−04	8268
NFBC86full	0.605(0.251)	0.0022	3639
SDC	1.009(0.708)	0.002	497
SHIP	0.574(0.268)	0.001	7159
WHI	0.471(0.289)	0.0019	21841
UKBiobank	−0.069(0.007)	0.0251	445360
Stage 1	**−0.063(0.006)**	**0.0258**	**554019**
Stage 2	**−0.064(0.006)**	**0.0254**	**686104**



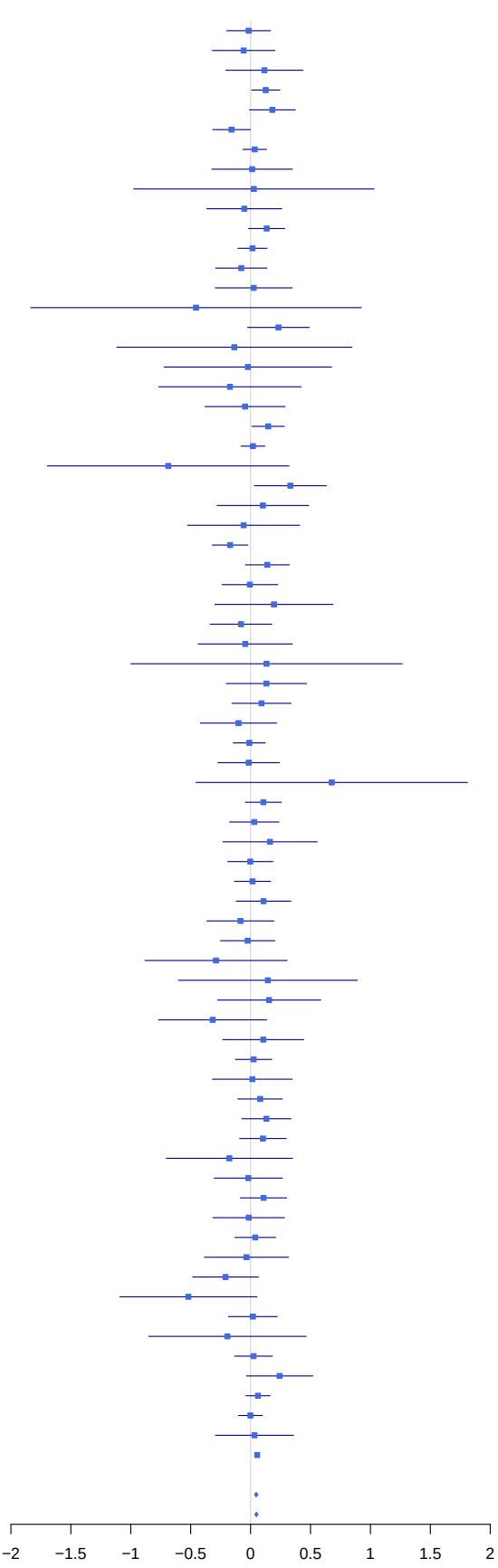
rs13039398, Minor allele/Other allele: A/G (PP)

Study	Beta(SE)	MAF	N
1958BC	−0.056(0.052)	0.0326	5861
ADDITION	−0.041(0.088)	0.0286	2306
AGES	−0.093(0.051)	0.0367	5526
AIRWAVE	−0.056(0.034)	0.0351	13102
ALSPAC	0.088(0.048)	0.036	6529
ARIC	−0.059(0.039)	0.032	10863
BRIGHTcases	−0.077(0.127)	0.0301	1098
BRIGHTcontrols	−0.14(0.327)	0.0379	132
CARDIA	−0.024(0.086)	0.0324	2175
CCHS	−0.021(0.046)	0.0294	8070
CGPS	−0.042(0.036)	0.0337	11783
CIHDS	0.091(0.111)	0.0303	1434
CROATA	−0.088(0.152)	0.0264	814
D2D2007	0.066(0.092)	0.0246	2580
DIABNORD	−0.179(0.123)	0.0367	912
DPS	0.561(0.196)	0.0337	416
DRSEXTRA	−0.032(0.153)	0.0277	740
EGCUT	−0.072(0.12)	0.0196	1785
EPIC	−0.043(0.033)	0.0299	15673
EPIC−Norfolk	−0.017(0.029)	0.035	17850
ERF	0.048(0.145)	0.0226	1152
FamHS	−0.167(0.07)	0.0314	3722
Fenland−CoreExome	0.009(0.115)	0.0381	1040
Fenland−GWAS	0.151(0.152)	0.027	1358
Fenland−OMICS	−0.03(0.045)	0.0305	8526
FHS	0.046(0.047)	0.0348	7495
FINRISK	−0.055(0.053)	0.0368	5152
FINRISK2007	−0.173(0.114)	0.0372	1088
FUSION	−0.095(0.063)	0.031	4237
GAPP	−0.099(0.109)	0.0221	1946
GLACIER	−0.045(0.118)	0.0401	922
GoDARTS CAD	0.111(0.105)	0.0363	1323
GoDARTS	−0.017(0.068)	0.032	3501
GRAPHIC	0.04(0.103)	0.0291	1887
GS	−0.028(0.038)	0.0378	9832
HEALTH	−0.091(0.06)	0.04	3674
HELIC−HA	0.149(0.161)	0.0222	944
HELIC−HP	−0.19(0.293)	0.0106	565
HRS	0.026(0.04)	0.0334	9621
HUNT	0.026(0.066)	0.0247	4735
INCIPE	−0.041(0.089)	0.0316	1995
INTER99	0.005(0.051)	0.0343	5983
InterAct−CoreExome	0.018(0.038)	0.0329	10915
InterAct−GWAS	−0.077(0.052)	0.0298	6675
INV SC	0.055(0.085)	0.0285	2461
INV UK	−0.068(0.069)	0.0339	3242
IPM	−0.289(0.119)	0.0281	1337
LBC1921	−0.394(0.21)	0.031	359
LBC1936	−0.085(0.145)	0.0296	783
LIFELINES	−0.162(0.097)	0.0277	1948
LRGP	0.051(0.096)	0.0245	2306
MDC	0.044(0.041)	0.0376	8268
MESA	−0.036(0.084)	0.0293	2505
METSIM	−0.038(0.04)	0.0417	8411
MORGAM	0.038(0.053)	0.0316	5757
NEO	−0.075(0.054)	0.0293	6115
NFBC66	0.043(0.095)	0.0418	1353
NFBC86full	−0.172(0.06)	0.0407	3639
OxBB	−0.037(0.058)	0.0349	4440
PIVUSULSAM	−0.184(0.089)	0.0318	1998
PPP	0.038(0.057)	0.0334	4766
PROSPER	0.002(0.097)	0.0385	1275
RS	−0.041(0.077)	0.0301	2875
SDC	−0.124(0.16)	0.0402	497
SHIP	0.023(0.051)	0.0277	7159
TwinsUK	−0.061(0.14)	0.0399	689
UKHLS	−0.041(0.045)	0.0342	7462
VEJLECASES	0.053(0.086)	0.0361	1996
WGHS	−0.016(0.027)	0.0326	21964
WHI	−0.068(0.027)	0.0321	21841
WOSCOPS	0.067(0.113)	0.0295	1337
UKBiobank	−0.024(0.006)	0.0333	445360
Stage 1	**−0.026(0.004)**	**0.0333**	**780080**
Stage 2	**−0.024(0.004)**	**0.0334**	**1133830**



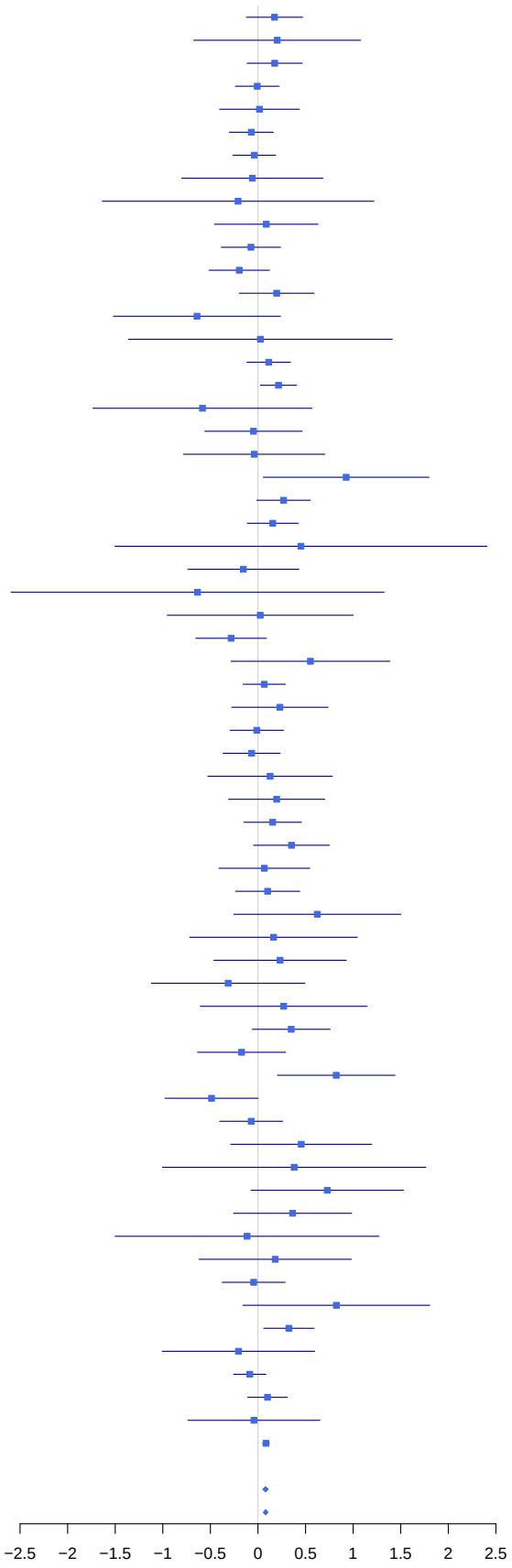
rs13141, Minor allele/Other allele: A/G (DBP)

Study	Beta(SE)	MAF	N
1958BC	−0.016(0.093)	0.0101	5864
ADDITION	−0.058(0.133)	0.0121	2307
AGES	0.116(0.164)	0.0034	5526
AIRWAVE	0.126(0.06)	0.0108	13102
ALSPAC	0.182(0.098)	0.0079	6529
ARIC	−0.159(0.08)	0.0073	10863
BIOVU	0.034(0.051)	0.0099	19885
BRIGHTcases	0.013(0.172)	0.015	1098
BRIGHTcontrols	0.027(0.512)	0.0152	132
CARDIA	−0.053(0.16)	0.0092	2175
CCHS	0.134(0.077)	0.0107	8070
CGPS	0.016(0.062)	0.0109	11783
CHS	−0.078(0.11)	0.0101	4109
CIHDS	0.026(0.164)	0.0126	1434
CROATA−KORCULA	−0.455(0.704)	0.0012	814
D2D2007	0.232(0.131)	0.0116	2580
DIABNORD	−0.136(0.501)	0.0022	912
DPS	−0.023(0.356)	0.0096	416
DRSEXTRA	−0.172(0.304)	0.0074	740
EGCUT	−0.046(0.171)	0.0098	1785
EPIC	0.147(0.069)	0.0066	15674
EPIC−Norfolk	0.02(0.051)	0.0111	17850
ERF	−0.687(0.514)	0.0017	1153
FamHS	0.332(0.153)	0.0066	3722
Fenland−CoreExome	0.102(0.195)	0.013	1040
Fenland−GWAS	−0.058(0.239)	0.0087	1358
Fenland−OMICS	−0.171(0.076)	0.0103	8526
FHS	0.14(0.094)	0.009	7495
FINRISK	−0.006(0.119)	0.0068	5153
FINRISK2007	0.195(0.252)	0.0074	1088
FUSION	−0.08(0.131)	0.007	4237
GAPP	−0.044(0.2)	0.0064	1946
GLACIER	0.133(0.578)	0.0016	922
GoDARTS CAD	0.132(0.171)	0.0132	1323
GoDARTS	0.091(0.126)	0.0091	3501
GRAPHIC	−0.101(0.162)	0.0106	1887
GS	−0.011(0.068)	0.011	9832
HEALTH	−0.015(0.131)	0.008	3674
HELIC−HP	0.677(0.578)	0.0027	565
HRS	0.107(0.077)	0.009	9621
HUNT	0.031(0.105)	0.0097	4735
INCIPE	0.162(0.201)	0.0063	1995
INTER99	−0.003(0.096)	0.009	5984
InterAct−CoreExome	0.016(0.077)	0.0079	10915
InterAct−GWAS	0.108(0.117)	0.006	6675
INV SC	−0.085(0.143)	0.0102	2461
INV UK	−0.024(0.116)	0.0117	3242
IPM	−0.289(0.303)	0.0041	1342
LBC1921	0.144(0.381)	0.0097	359
LBC1936	0.155(0.22)	0.0121	783
LIFELINES	−0.316(0.231)	0.0049	1948
LRGP	0.106(0.173)	0.0074	2306
MDC	0.025(0.078)	0.0102	8268
MESA	0.015(0.17)	0.007	2505
METSIM	0.08(0.095)	0.0065	8411
MORGAM	0.132(0.104)	0.0076	5757
NEO	0.103(0.099)	0.0084	6115
NFBC66	−0.177(0.269)	0.0052	1353
NFBC86full	−0.019(0.145)	0.0063	3639
OxBB	0.108(0.099)	0.0114	4440
PIVUSULSAM	−0.016(0.152)	0.011	1998
PPP	0.039(0.087)	0.0143	4766
PROSPER	−0.034(0.179)	0.0125	1275
RS	−0.209(0.14)	0.009	2875
SDC	−0.519(0.292)	0.012	498
SHIP	0.019(0.104)	0.0064	7160
TwinsUK	−0.193(0.335)	0.0065	689
UKHLS	0.025(0.081)	0.0104	7462
VEJLECASES	0.242(0.142)	0.0117	2002
WGHS	0.062(0.051)	0.0089	21964
WHI	−0.002(0.051)	0.0089	21841
WOSCOPS	0.033(0.166)	0.0138	1337
UKBiobank	0.055(0.01)	0.0113	445360
Stage 1	**0.047(0.008)**	**0.0106**	**803151**
Stage 2	**0.048(0.007)**	**0.0101**	**1156950**



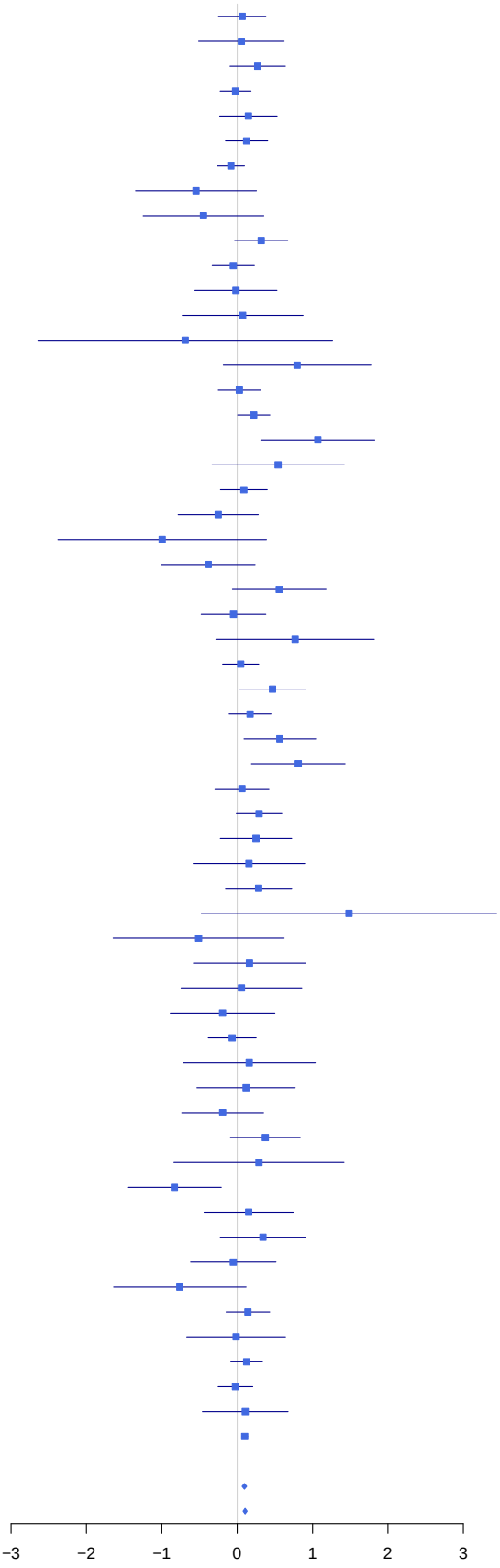
rs141325069, Minor allele/Other allele: A/G (SBP)

Study	Beta(SE)	MAF	N
1958BC	0.174(0.151)	0.0038	5864
ADDITION	0.202(0.447)	0.0011	2307
AGES	0.176(0.148)	0.0042	5526
AIRWAVE	−0.008(0.117)	0.0027	13102
ALSPAC	0.016(0.214)	0.0017	6529
ARIC	−0.07(0.118)	0.0032	10864
BIOVU	−0.039(0.115)	0.0019	19885
BRIGHTcases	−0.059(0.379)	0.0032	1098
BRIGHTcontrols	−0.209(0.728)	0.0076	132
CARDIA	0.087(0.277)	0.003	2175
CCHS	−0.074(0.159)	0.0024	8070
CGPS	−0.196(0.162)	0.0016	11784
CHS	0.197(0.201)	0.003	4113
CIHDS	−0.641(0.448)	0.0017	1436
DIABNORD	0.025(0.707)	0.0011	912
EPIC	0.113(0.117)	0.0023	15676
EPIC−Norfolk	0.216(0.097)	0.003	17850
ERF	−0.583(0.587)	0.0013	1153
FamHS	−0.047(0.261)	0.0023	3722
Fenland−CoreExome	−0.04(0.379)	0.0034	1040
Fenland−GWAS	0.927(0.444)	0.0023	1358
Fenland−OMICS	0.269(0.143)	0.0029	8526
FHS	0.155(0.137)	0.0043	7495
FINRISK	0.451(0.997)	1e−04	5152
GAPP	−0.154(0.298)	0.0028	1947
GLACIER	−0.635(1)	5e−04	922
GoDARTS CAD	0.024(0.499)	0.0015	1323
GoDARTS	−0.282(0.19)	0.0037	3501
GRAPHIC	0.551(0.426)	0.0016	1887
GS	0.066(0.113)	0.004	9832
HEALTH	0.23(0.259)	0.002	3674
HRS	−0.013(0.143)	0.0025	9621
HUNT	−0.067(0.153)	0.0045	4735
INCIPE	0.128(0.334)	0.0023	1995
INTER99	0.196(0.258)	0.0013	5986
InterAct−CoreExome	0.155(0.154)	0.0019	10915
InterAct−GWAS	0.352(0.204)	0.002	6675
INV SC	0.067(0.243)	0.0035	2461
INV UK	0.101(0.172)	0.0052	3242
IPM	0.624(0.448)	0.0019	1337
LBC1921	0.163(0.45)	0.007	359
LBC1936	0.232(0.355)	0.0051	783
LIFELINES	−0.314(0.412)	0.0015	1948
LRGP	0.27(0.447)	0.0011	2306
MDC	0.349(0.209)	0.0014	8268
MESA	−0.172(0.236)	0.0036	2505
MORGAM	0.822(0.315)	9e−04	5757
NEO	−0.488(0.25)	0.0013	6117
OxBB	−0.072(0.17)	0.0039	4440
PIVUSULSAM	0.455(0.378)	0.0018	1998
PPP	0.38(0.706)	2e−04	4766
PROSPER	0.728(0.409)	0.0024	1275
RS	0.364(0.317)	0.0017	2875
SDC	−0.115(0.708)	0.002	498
SDR−ANDIS	0.181(0.408)	0.0011	2636
SHIP	−0.045(0.169)	0.0024	7161
TwinsUK	0.824(0.501)	0.0029	689
UKHLS	0.325(0.135)	0.0037	7462
VEJLECASES	−0.204(0.409)	0.0015	1996
WGHS	−0.086(0.087)	0.003	21964
WHI	0.1(0.107)	0.002	21841
WOSCOPS	−0.043(0.354)	0.003	1337
UKBiobank	0.084(0.018)	0.0034	445360
Stage 1	**0.079(0.014)**	**0.0032**	**780163**
Stage 2	**0.081(0.012)**	**0.0031**	**1134260**



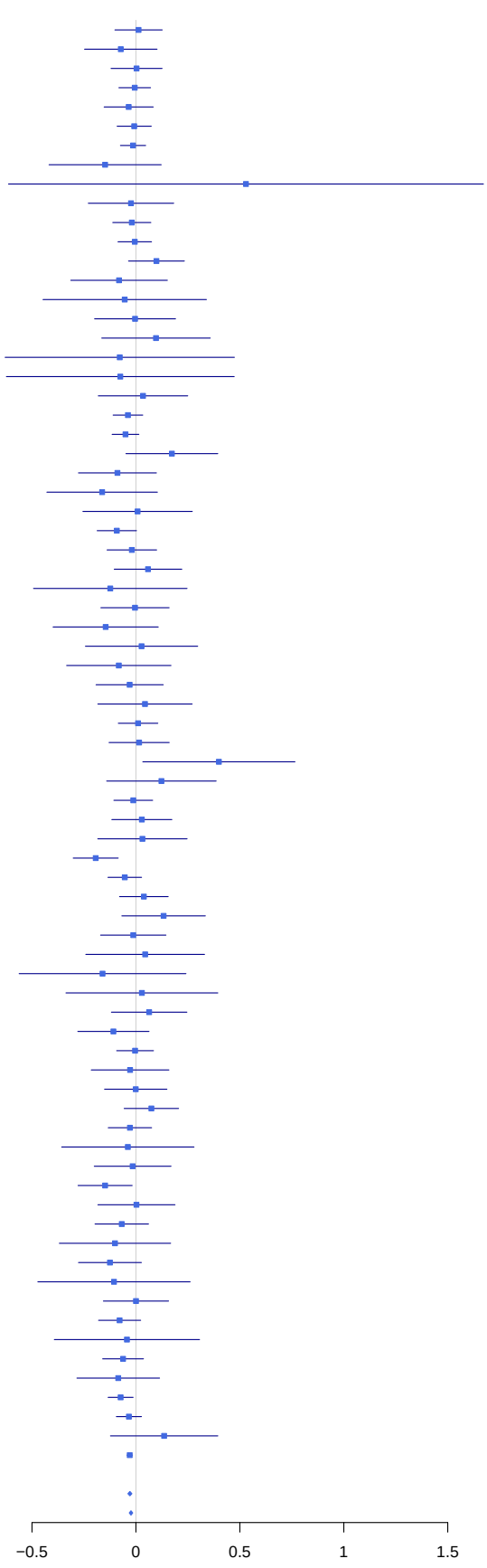
rs143057152, Minor allele/Other allele: T/C (SBP)

Study	Beta(SE)	MAF	N
1958BC	0.066(0.16)	0.0033	5864
ADDITION	0.055(0.289)	0.0026	2307
AGES	0.272(0.187)	0.0026	5526
AIRWAVE	−0.021(0.105)	0.0034	13102
ALSPAC	0.149(0.195)	0.0021	6529
ARIC	0.125(0.143)	0.0023	10864
BIOVU	−0.084(0.092)	0.003	19885
BRIGHTcases	−0.546(0.409)	0.0027	1098
CARDIA	−0.447(0.408)	0.0014	2175
CCHS	0.318(0.18)	0.0019	8070
CGPS	−0.052(0.143)	0.002	11784
CHS	−0.017(0.278)	0.0016	4113
CIHDS	0.072(0.409)	0.0021	1436
D2D2007	−0.69(0.997)	2e−04	2580
EGCUT	0.795(0.5)	0.0011	1785
EPIC	0.028(0.143)	0.0016	15676
EPIC−Norfolk	0.22(0.109)	0.0025	17850
FamHS	1.069(0.386)	9e−04	3722
Fenland−CoreExome	0.543(0.448)	0.0024	1040
Fenland−OMICS	0.088(0.158)	0.0023	8526
FHS	−0.252(0.271)	0.001	7495
FINRISK	−0.995(0.706)	2e−04	5152
GAPP	−0.384(0.317)	0.0026	1947
GoDARTS CAD	0.557(0.317)	0.0038	1323
GoDARTS	−0.049(0.219)	0.003	3501
GRAPHIC	0.768(0.536)	0.0011	1887
GS	0.046(0.122)	0.0035	9832
HEALTH	0.469(0.224)	0.0027	3674
HRS	0.171(0.142)	0.0025	9621
HUNT	0.566(0.243)	0.0018	4735
INCIPE	0.81(0.317)	0.0025	1995
INTER99	0.063(0.183)	0.0025	5986
InterAct−CoreExome	0.29(0.154)	0.0019	10915
InterAct−GWAS	0.249(0.242)	0.0014	6675
INV SC	0.156(0.378)	0.0014	2461
INV UK	0.284(0.224)	0.0031	3242
IPM	1.483(1)	4e−04	1337
LBC1921	−0.512(0.579)	0.0042	359
LBC1936	0.162(0.379)	0.0045	783
LIFELINES	0.056(0.409)	0.0015	1948
LRGP	−0.194(0.354)	0.0017	2306
MDC	−0.066(0.162)	0.0022	8268
MESA	0.159(0.447)	0.001	2505
MORGAM	0.118(0.333)	8e−04	5757
NEO	−0.193(0.277)	0.0011	6117
OxBB	0.373(0.236)	0.002	4440
PIVUSULSAM	0.289(0.576)	8e−04	1998
PROSPER	−0.833(0.317)	0.0039	1275
RS	0.152(0.302)	0.0019	2875
SDR−ANDIS	0.341(0.289)	0.0023	2636
SHIP	−0.052(0.289)	8e−04	7161
TwinsUK	−0.761(0.448)	0.0036	689
UKHLS	0.142(0.148)	0.0031	7462
VEJLECASES	−0.014(0.334)	0.0023	1996
WGHS	0.125(0.107)	0.002	21964
WHI	−0.023(0.117)	0.0017	21841
WOSCOPS	0.107(0.29)	0.0045	1337
UKBiobank	0.1(0.019)	0.0028	445360
Stage 1	**0.096(0.016)**	**0.0027**	**774787**
Stage 2	**0.105(0.014)**	**0.0026**	**1128880**



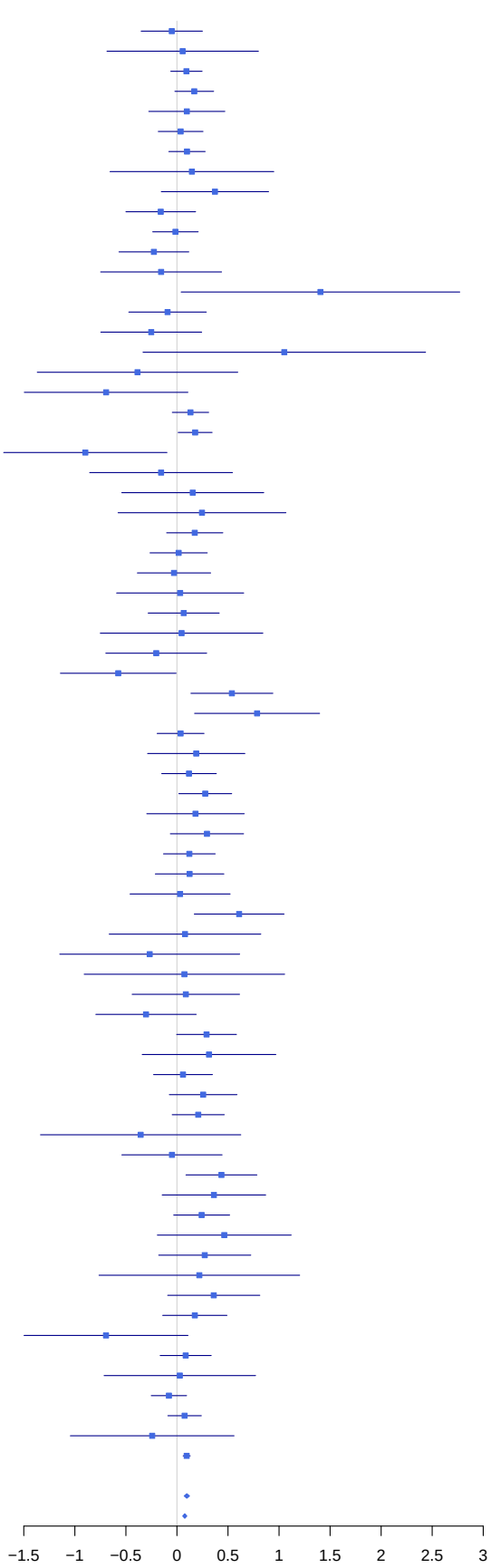
rs144867634, Minor allele/Other allele: C/T (DBP)

Study	Beta(SE)	MAF	N
1958BC	0.013(0.058)	0.026	5864
ADDITION	−0.073(0.089)	0.0277	2307
AGES	0.003(0.063)	0.0241	5526
AIRWAVE	−0.006(0.039)	0.0258	13102
ALSPAC	−0.035(0.06)	0.0224	6529
ARIC	−0.008(0.042)	0.0261	10863
BIOVU	−0.014(0.031)	0.027	19885
BRIGHTcases	−0.148(0.138)	0.0241	1098
BRIGHTcontrols	0.529(0.583)	0.0114	132
CARDIA	−0.024(0.105)	0.0214	2175
CCHS	−0.02(0.047)	0.0287	8070
CGPS	−0.006(0.041)	0.0259	11783
CHS	0.099(0.069)	0.0265	4109
CIHDS	−0.081(0.119)	0.0262	1434
CROATA−KORCULA	−0.054(0.201)	0.016	814
D2D2007	−0.004(0.099)	0.0207	2580
DIABNORD	0.096(0.133)	0.0318	912
DPS	−0.078(0.281)	0.0156	416
DRSEXTRA	−0.075(0.28)	0.0088	740
EGCUT	0.034(0.11)	0.0238	1785
EPIC	−0.039(0.036)	0.0241	15674
EPIC−Norfolk	−0.05(0.033)	0.0269	17850
ERF	0.173(0.113)	0.0386	1153
FamHS	−0.089(0.096)	0.0169	3722
Fenland−CoreExome	−0.163(0.136)	0.0255	1040
Fenland−GWAS	0.008(0.134)	0.0284	1358
Fenland−OMICS	−0.092(0.048)	0.026	8526
FHS	−0.02(0.061)	0.0212	7495
FINRISK	0.058(0.083)	0.0144	5153
FINRISK2007	−0.123(0.188)	0.0133	1088
FUSION	−0.005(0.084)	0.0172	4237
GAPP	−0.146(0.129)	0.0152	1946
GLACIER	0.027(0.138)	0.0304	922
GoDARTS CAD	−0.082(0.128)	0.0234	1323
GoDARTS	−0.03(0.082)	0.0221	3501
GRAPHIC	0.044(0.116)	0.0215	1887
GS	0.01(0.049)	0.0225	9832
HEALTH	0.015(0.074)	0.0252	3674
HELIC−HA	0.399(0.187)	0.0159	944
HELIC−HP	0.123(0.134)	0.0549	565
HRS	−0.013(0.048)	0.0235	9621
HUNT	0.028(0.074)	0.0195	4735
INCIPE	0.031(0.11)	0.0218	1995
INTER99	−0.193(0.055)	0.0288	5984
InterAct−CoreExome	−0.054(0.041)	0.0277	10915
InterAct−GWAS	0.038(0.06)	0.0248	6675
INV SC	0.133(0.102)	0.0197	2461
INV UK	−0.013(0.08)	0.0245	3242
IPM	0.044(0.146)	0.0183	1342
LBC1921	−0.161(0.205)	0.0292	359
LBC1936	0.029(0.186)	0.0192	783
LIFELINES	0.064(0.093)	0.0303	1948
LRGP	−0.108(0.087)	0.0293	2306
MDC	−0.004(0.045)	0.0306	8268
MESA	−0.028(0.095)	0.0226	2505
METSIM	−0.001(0.077)	0.0106	8411
MORGAM	0.074(0.067)	0.0193	5757
NEO	−0.029(0.053)	0.0295	6115
NFBC66	−0.039(0.162)	0.0144	1353
NFBC86full	−0.016(0.094)	0.0154	3639
OxBB	−0.148(0.066)	0.0255	4440
PIVUSULSAM	0.003(0.095)	0.0285	1998
PPP	−0.068(0.066)	0.025	4766
PROSPER	−0.101(0.137)	0.022	1275
RS	−0.125(0.077)	0.0299	2875
SDC	−0.106(0.187)	0.0261	498
SDR−ANDIS	0(0.08)	0.0303	2636
SHIP	−0.078(0.052)	0.0272	7160
TwinsUK	−0.043(0.178)	0.0239	689
UKHLS	−0.062(0.05)	0.0269	7462
VEJLECASES	−0.085(0.101)	0.0245	2002
WGHS	−0.074(0.031)	0.0247	21964
WHI	−0.034(0.031)	0.0248	21841
WOSCOPS	0.136(0.132)	0.0224	1337
UKBiobank	−0.03(0.007)	0.0255	445360
Stage 1	**−0.029(0.005)**	**0.0254**	**806731**
Stage 2	**−0.024(0.004)**	**0.0252**	**1160530**



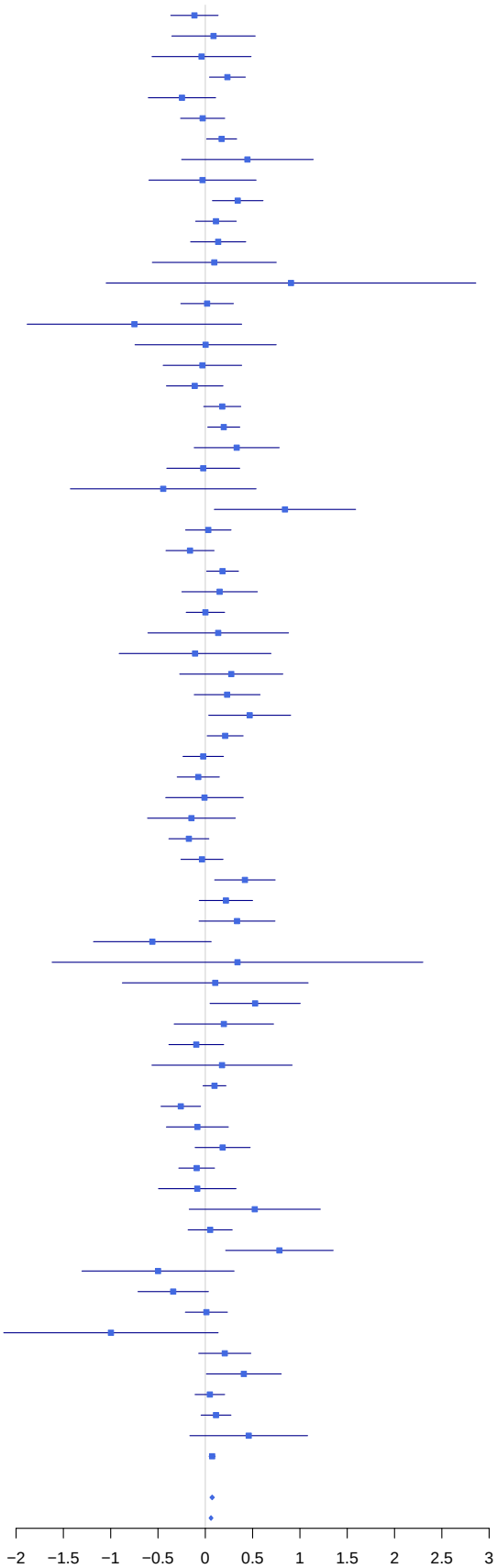
rs145072852, Minor allele/Other allele: T/C (PP)

Study	Beta(SE)	MAF	N
1958BC	−0.051(0.153)	0.0037	5861
ADDITION	0.056(0.378)	0.0015	2306
AGES	0.093(0.078)	0.0153	5526
AIRWAVE	0.17(0.097)	0.0041	13102
ALSPAC	0.097(0.19)	0.0021	6529
ARIC	0.036(0.112)	0.0037	10863
BIOVU	0.098(0.091)	0.0031	19885
BRIGHTcases	0.147(0.409)	0.0027	1098
CARDIA	0.372(0.268)	0.0032	2175
CCHS	−0.159(0.174)	0.002	8070
CGPS	−0.015(0.114)	0.0033	11783
CHS	−0.226(0.174)	0.004	4109
CIHDS	−0.155(0.302)	0.0031	1434
CROATA	1.406(0.696)	0.0012	814
D2D2007	−0.092(0.194)	0.0052	2580
DIABNORD	−0.252(0.252)	0.0088	912
DPS	1.051(0.706)	0.0024	416
DRSEXTRA	−0.386(0.501)	0.0027	740
EGCUT	−0.694(0.409)	0.0017	1785
EPIC	0.132(0.091)	0.0039	15673
EPIC−Norfolk	0.178(0.085)	0.0039	17850
ERF	−0.897(0.408)	0.0026	1152
FamHS	−0.155(0.357)	0.0011	3722
Fenland−CoreExome	0.155(0.355)	0.0038	1040
Fenland−GWAS	0.245(0.419)	0.0023	1358
Fenland−OMICS	0.174(0.14)	0.003	8526
FHS	0.017(0.143)	0.0039	7495
FINRISK	−0.029(0.183)	0.0029	5152
FINRISK2007	0.032(0.317)	0.0046	1088
FUSION	0.066(0.177)	0.0038	4237
GAPP	0.045(0.406)	0.0015	1946
GLACIER	−0.203(0.252)	0.0087	922
GoDARTS CAD	−0.575(0.289)	0.0045	1323
GoDARTS	0.538(0.205)	0.0034	3501
GRAPHIC	0.785(0.312)	0.0029	1887
GS	0.036(0.117)	0.0038	9832
HEALTH	0.189(0.243)	0.0023	3674
HRS	0.118(0.136)	0.0028	9621
HUNT	0.277(0.132)	0.0061	4735
INCIPE	0.182(0.243)	0.0043	1995
INTER99	0.294(0.183)	0.0025	5983
InterAct−CoreExome	0.122(0.129)	0.0027	10915
InterAct−GWAS	0.124(0.171)	0.0028	6675
INV SC	0.031(0.25)	0.0028	2461
INV UK	0.609(0.224)	0.0031	3242
IPM	0.079(0.379)	0.0026	1337
LBC1921	−0.267(0.45)	0.007	359
LBC1936	0.073(0.501)	0.0026	783
LIFELINES	0.087(0.268)	0.0036	1948
LRGP	−0.303(0.251)	0.0035	2306
MDC	0.29(0.149)	0.0027	8268
MESA	0.314(0.334)	0.0018	2505
METSIM	0.059(0.147)	0.0027	8411
MORGAM	0.257(0.169)	0.003	5757
NEO	0.209(0.13)	0.0049	6115
NFBC66	−0.356(0.501)	0.0015	1353
NFBC86full	−0.049(0.251)	0.0022	3639
OxBB	0.436(0.177)	0.0036	4440
PIVUSULSAM	0.362(0.259)	0.0038	1998
PPP	0.242(0.14)	0.0055	4766
PROSPER	0.464(0.334)	0.0035	1275
RS	0.272(0.23)	0.0033	2875
SDC	0.219(0.501)	0.004	497
SDR−ANDIS	0.36(0.23)	0.0036	2634
SHIP	0.175(0.161)	0.0027	7159
TwinsUK	−0.695(0.41)	0.0044	689
UKHLS	0.086(0.128)	0.0042	7462
VEJLECASES	0.028(0.378)	0.0018	1996
WGHS	−0.079(0.088)	0.0029	21964
WHI	0.075(0.084)	0.0033	21841
WOSCOPS	−0.242(0.409)	0.0022	1337
UKBiobank	0.095(0.018)	0.0034	445360
Stage 1	**0.097(0.013)**	**0.0038**	**805067**
Stage 2	**0.077(0.01)**	**0.007**	**1158820**



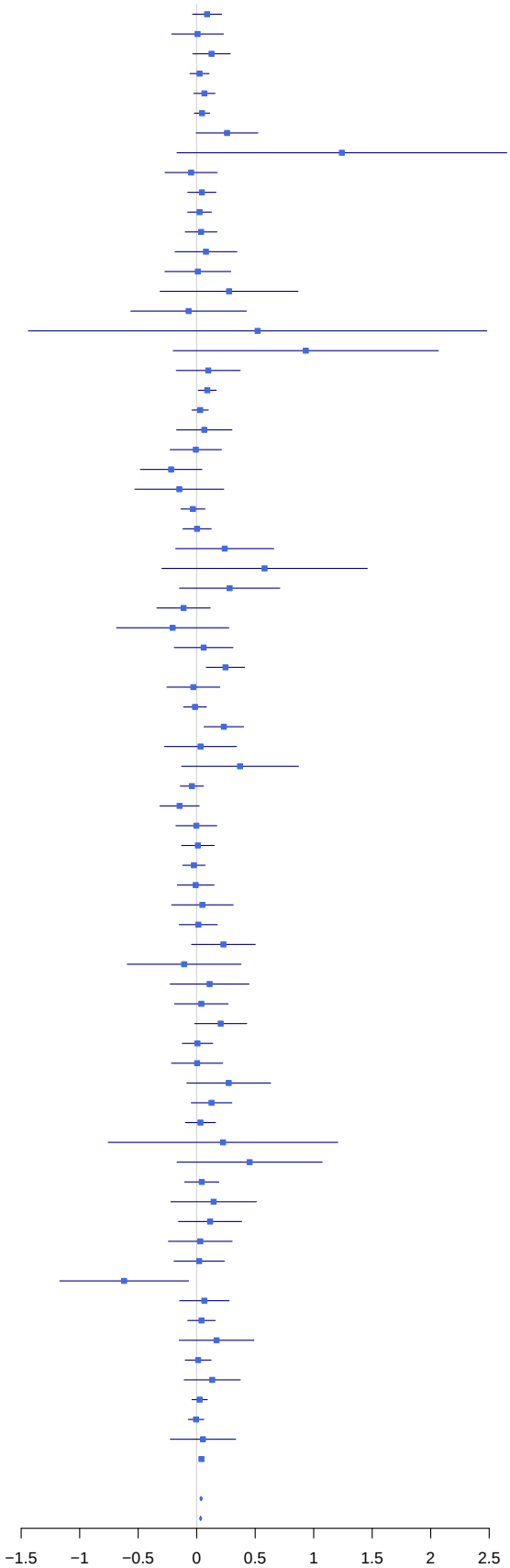
rs145502455, Minor allele/Other allele: A/G (SBP)

Study	Beta(SE)	MAF	N
1958BC	−0.115(0.128)	0.0053	5864
ADDITION	0.087(0.225)	0.0043	2307
AGES	−0.04(0.267)	0.0013	5526
AIRWAVE	0.234(0.097)	0.0041	13102
ALSPAC	−0.247(0.181)	0.0024	6529
ARIC	−0.028(0.119)	0.0033	10864
BIOVU	0.173(0.081)	0.0039	19885
BRIGHTcases	0.445(0.355)	0.0036	1098
CARDIA	−0.03(0.289)	0.0028	2175
CCHS	0.343(0.136)	0.0033	8070
CGPS	0.113(0.11)	0.0035	11784
CHS	0.136(0.149)	0.0057	4113
CIHDS	0.095(0.334)	0.0031	1436
CROATA−KORCULA	0.906(0.997)	6e−04	814
D2D2007	0.019(0.142)	0.0101	2580
DIABNORD	−0.749(0.578)	0.0016	912
DPS	0.003(0.381)	0.0084	416
DRSEXTRA	−0.03(0.212)	0.0155	740
EGCUT	−0.112(0.152)	0.0123	1785
EPIC	0.179(0.1)	0.0031	15676
EPIC−Norfolk	0.195(0.086)	0.0037	17850
ERF	0.332(0.229)	0.0087	1153
FamHS	−0.022(0.197)	0.0039	3722
Fenland−CoreExome	−0.445(0.501)	0.0019	1040
Fenland−GWAS	0.842(0.381)	0.0036	1358
Fenland−OMICS	0.032(0.123)	0.0039	8526
FHS	−0.162(0.13)	0.0046	7495
FINRISK	0.182(0.086)	0.0136	5152
FINRISK2007	0.151(0.204)	0.0115	1088
FUSION	0.001(0.104)	0.0112	4237
GAPP	0.136(0.379)	0.0018	1947
GLACIER	−0.108(0.409)	0.0033	922
GoDARTS CAD	0.274(0.278)	0.0049	1323
GoDARTS	0.231(0.178)	0.0046	3501
GRAPHIC	0.469(0.221)	0.0064	1887
GS	0.21(0.097)	0.0055	9832
HEALTH	−0.022(0.109)	0.0117	3674
HRS	−0.074(0.114)	0.004	9621
HUNT	−0.009(0.209)	0.0024	4735
INCIPE	−0.146(0.237)	0.0045	1995
INTER99	−0.174(0.108)	0.0081	5986
InterAct−CoreExome	−0.035(0.113)	0.0036	10915
InterAct−GWAS	0.419(0.163)	0.0034	6675
INV SC	0.218(0.144)	0.0098	2461
INV UK	0.335(0.205)	0.0034	3242
IPM	−0.56(0.317)	0.0037	1337
LBC1921	0.34(1)	0.0014	359
LBC1936	0.105(0.501)	0.0026	783
LIFELINES	0.527(0.243)	0.0044	1948
LRGP	0.196(0.268)	0.003	2306
MDC	−0.095(0.148)	0.0028	8268
MESA	0.177(0.378)	0.0014	2505
METSIM	0.097(0.062)	0.0169	8411
MORGAM	−0.259(0.107)	0.0076	5757
NEO	−0.084(0.167)	0.0029	6117
NFBC66	0.183(0.148)	0.0174	1353
NFBC86full	−0.091(0.096)	0.0154	3639
OxBB	−0.085(0.209)	0.0026	4440
PIVUSULSAM	0.523(0.353)	0.002	1998
PPP	0.051(0.119)	0.0077	4766
PROSPER	0.783(0.29)	0.0047	1275
SDC	−0.5(0.41)	0.006	498
SDR−ANDIS	−0.339(0.19)	0.0049	2636
SHIP	0.011(0.113)	0.0054	7161
TwinsUK	−0.997(0.578)	0.0022	689
UKHLS	0.206(0.141)	0.0034	7462
VEJLECASES	0.407(0.202)	0.0063	1996
WGHS	0.048(0.08)	0.0036	21964
WHI	0.113(0.081)	0.0035	21841
WOSCOPS	0.459(0.317)	0.0037	1337
UKBiobank	0.072(0.016)	0.004	445360
Stage 1	**0.072(0.012)**	**0.0054**	**802219**
Stage 2	**0.061(0.01)**	**0.0051**	**1156310**



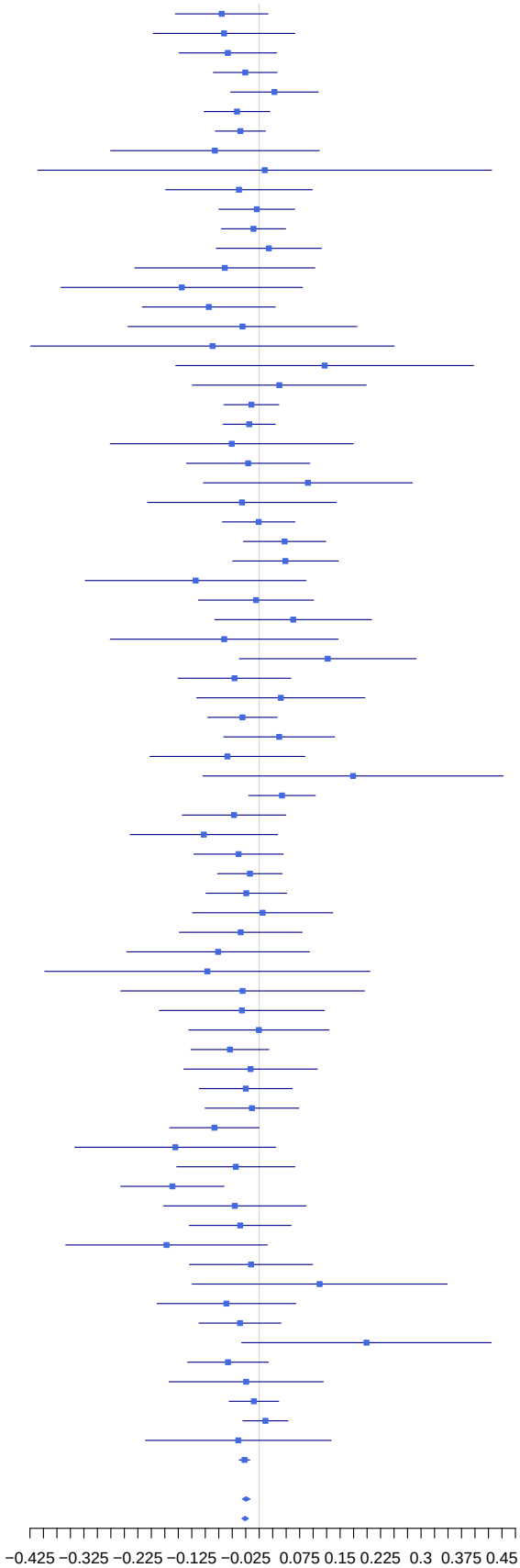
rs150843673, Minor allele/Other allele: T/G (DBP)

Study	Beta(SE)	MAF	N
1958BC	0.089(0.063)	0.0216	5864
ADDITION	0.008(0.113)	0.0178	2307
AGES	0.127(0.082)	0.0139	5526
AIRWAVE	0.025(0.042)	0.0222	13102
ARIC	0.066(0.046)	0.0214	10863
BIOVU	0.046(0.034)	0.0226	19885
BRIGHTcases	0.259(0.134)	0.0255	1098
BRIGHTcontrols	1.241(0.719)	0.0076	132
CARDIA	−0.047(0.114)	0.0179	2175
CCHS	0.044(0.061)	0.0163	8070
CGPS	0.025(0.052)	0.0163	11783
CHS	0.038(0.069)	0.026	4109
CIHDS	0.079(0.135)	0.0192	1434
CROATA−KORCULA	0.01(0.144)	0.0332	814
D2D2007	0.277(0.301)	0.0021	2580
DIABNORD	−0.069(0.252)	0.0088	912
DPS	0.521(1)	0.0012	416
DRSEXTRA	0.932(0.578)	0.002	740
EGCUT	0.099(0.139)	0.0148	1785
EPIC	0.091(0.039)	0.021	15674
EPIC−Norfolk	0.03(0.036)	0.0227	17850
ERF	0.065(0.121)	0.0356	1153
FamHS	−0.007(0.112)	0.0126	3722
Fenland−CoreExome	−0.218(0.134)	0.025	1040
Fenland−GWAS	−0.148(0.194)	0.0211	1358
Fenland−OMICS	−0.032(0.052)	0.0222	8526
FHS	0.003(0.062)	0.0201	7495
FINRISK	0.239(0.214)	0.0021	5153
FINRISK2007	0.58(0.448)	0.0023	1088
FUSION	0.282(0.219)	0.0025	4237
GAPP	−0.112(0.116)	0.0185	1946
GLACIER	−0.205(0.245)	0.0092	922
GoDARTS CAD	0.059(0.128)	0.0234	1323
GoDARTS	0.246(0.084)	0.0203	3501
GRAPHIC	−0.028(0.115)	0.0215	1887
GS	−0.014(0.05)	0.0205	9832
HEALTH	0.232(0.087)	0.0186	3674
HELIC−HA	0.033(0.157)	0.0228	944
HELIC−HP	0.371(0.255)	0.0142	565
HRS	−0.041(0.05)	0.0212	9621
HUNT	−0.146(0.086)	0.0144	4735
INCIPE	−0.003(0.089)	0.0316	1995
INTER99	0.011(0.071)	0.0171	5984
InterAct−CoreExome	−0.024(0.049)	0.0196	10915
InterAct−GWAS	−0.008(0.08)	0.02	6675
INV SC	0.049(0.134)	0.0116	2461
INV UK	0.014(0.083)	0.0231	3242
IPM	0.228(0.139)	0.0194	1342
LBC1921	−0.107(0.248)	0.0237	359
LBC1936	0.111(0.172)	0.0211	783
LIFELINES	0.04(0.117)	0.019	1948
LRGP	0.205(0.114)	0.0165	2306
MDC	0.007(0.067)	0.0137	8268
MESA	0.004(0.112)	0.0162	2505
METSIM	0.274(0.183)	0.0018	8411
MORGAM	0.127(0.089)	0.0109	5757
NEO	0.032(0.066)	0.0195	6115
NFBC66	0.225(0.501)	0.0015	1353
NFBC86full	0.453(0.316)	0.0014	3639
OxBB	0.043(0.074)	0.0209	4440
PIVUSULSAM	0.145(0.187)	0.0073	1998
PPP	0.115(0.138)	0.0057	4766
PROSPER	0.031(0.139)	0.0212	1275
RS	0.021(0.109)	0.015	2875
SDC	−0.62(0.281)	0.0131	498
SDR−ANDIS	0.066(0.108)	0.0169	2636
SHIP	0.041(0.06)	0.0198	7160
TwinsUK	0.17(0.163)	0.029	689
UKHLS	0.013(0.056)	0.0216	7462
VEJLECASES	0.133(0.122)	0.0167	2002
WGHS	0.025(0.033)	0.0209	21964
WHI	−0.005(0.034)	0.0206	21841
WOSCOPS	0.054(0.143)	0.0191	1337
UKBiobank	0.041(0.007)	0.0219	445360
Stage 1	**0.038(0.006)**	**0.0213**	**800202**
Stage 2	**0.034(0.005)**	**0.0213**	**1154000**



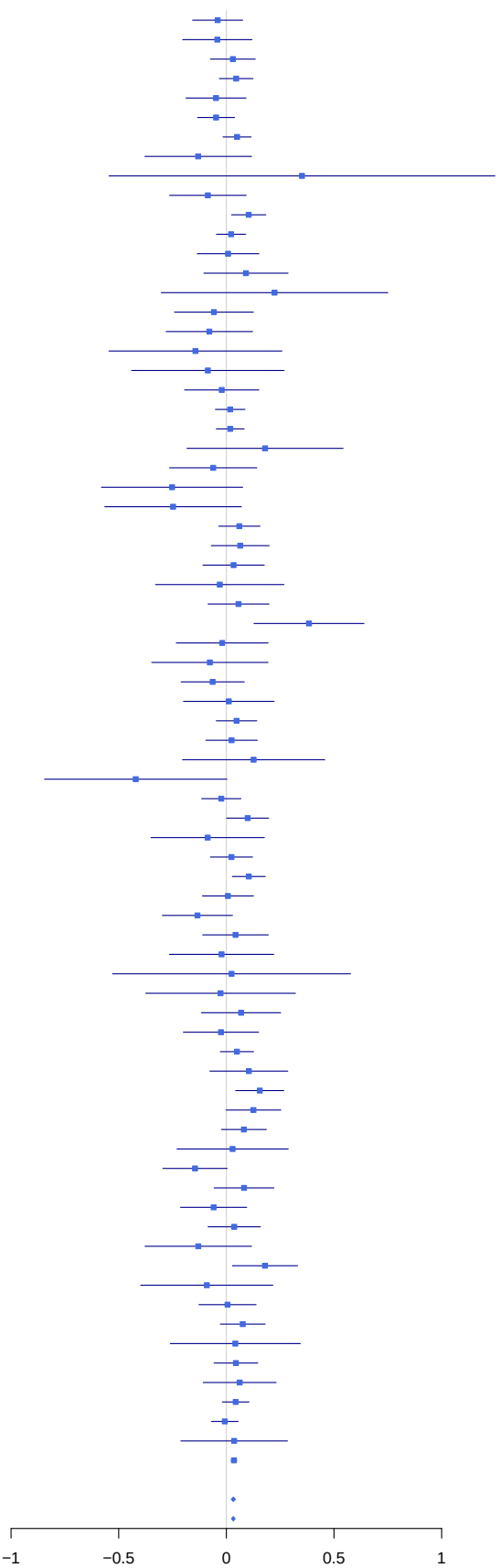
rs16859180, Minor allele/Other allele: T/C (DBP)

Study	Beta(SE)	MAF	N
1958BC	−0.07(0.044)	0.0501	5864
ADDITION	−0.065(0.067)	0.0505	2307
AGES	−0.058(0.046)	0.0462	5526
AIRWAVE	−0.026(0.03)	0.0506	13102
ALSPAC	0.028(0.042)	0.0506	6529
ARIC	−0.041(0.031)	0.0543	10863
BIOVU	−0.035(0.024)	0.0479	19885
BRIGHTcases	−0.082(0.099)	0.0464	1098
BRIGHTcontrols	0.01(0.215)	0.0947	132
CARDIA	−0.038(0.069)	0.0506	2175
CCHS	−0.004(0.036)	0.0532	8070
CGPS	−0.011(0.03)	0.0515	11783
CHS	0.018(0.05)	0.0532	4109
CIHDS	−0.064(0.085)	0.0502	1434
CROATA−KORCULA	−0.144(0.114)	0.0455	814
D2D2007	−0.093(0.063)	0.0543	2580
DIABNORD	−0.031(0.108)	0.0493	912
DPS	−0.087(0.172)	0.0445	416
DRSEXTRA	0.121(0.141)	0.0351	740
EGCUT	0.037(0.082)	0.0415	1785
EPIC	−0.015(0.026)	0.0526	15674
EPIC−Norfolk	−0.019(0.025)	0.0486	17850
ERF	−0.051(0.115)	0.0369	1153
FamHS	−0.02(0.058)	0.0462	3722
Fenland−CoreExome	0.09(0.099)	0.0529	1040
Fenland−GWAS	−0.032(0.089)	0.0493	1358
Fenland−OMICS	−0.001(0.034)	0.0521	8526
FHS	0.047(0.039)	0.0525	7495
FINRISK	0.049(0.05)	0.0408	5153
FINRISK2007	−0.118(0.104)	0.0455	1088
FUSION	−0.006(0.054)	0.0425	4237
GAPP	0.063(0.074)	0.0511	1946
GLACIER	−0.065(0.108)	0.0521	922
GoDARTS CAD	0.127(0.084)	0.0556	1323
GoDARTS	−0.046(0.053)	0.0527	3501
GRAPHIC	0.04(0.08)	0.0522	1887
GS	−0.031(0.033)	0.0569	9832
HEALTH	0.037(0.052)	0.0546	3674
HELIC−HA	−0.059(0.073)	0.1102	944
HELIC−HP	0.174(0.142)	0.0416	565
HRS	0.042(0.032)	0.0553	9621
HUNT	−0.047(0.049)	0.0447	4735
INCIPE	−0.103(0.07)	0.0551	1995
INTER99	−0.038(0.042)	0.0535	5984
InterAct−CoreExome	−0.017(0.031)	0.0525	10915
InterAct−GWAS	−0.024(0.038)	0.0544	6675
INV SC	0.006(0.066)	0.0484	2461
INV UK	−0.034(0.058)	0.0492	3242
IPM	−0.076(0.086)	0.0555	1342
LBC1921	−0.096(0.154)	0.0641	359
LBC1936	−0.031(0.115)	0.0517	783
LIFELINES	−0.032(0.078)	0.0444	1948
LRGP	−0.001(0.066)	0.0538	2306
MDC	−0.054(0.037)	0.0472	8268
MESA	−0.016(0.063)	0.0531	2505
METSIM	−0.025(0.044)	0.0349	8411
MORGAM	−0.013(0.044)	0.0474	5757
NEO	−0.083(0.042)	0.0479	6115
NFBC66	−0.156(0.095)	0.0414	1353
NFBC86full	−0.043(0.056)	0.0458	3639
OxBB	−0.161(0.049)	0.049	4440
PIVUSULSAM	−0.045(0.067)	0.0571	1998
PPP	−0.035(0.048)	0.0504	4766
PROSPER	−0.172(0.095)	0.0467	1275
RS	−0.015(0.058)	0.0539	2875
SDC	0.112(0.121)	0.0693	498
SDR−ANDIS	−0.061(0.066)	0.0465	2636
SHIP	−0.036(0.039)	0.052	7160
TwinsUK	0.199(0.118)	0.0552	689
UKHLS	−0.058(0.038)	0.0497	7462
VEJLECASES	−0.024(0.073)	0.05	2002
WGHS	−0.01(0.023)	0.0513	21964
WHI	0.011(0.021)	0.053	21841
WOSCOPS	−0.039(0.088)	0.0524	1337
UKBiobank	−0.027(0.005)	0.048	445360
Stage 1	**−0.024(0.004)**	**0.0493**	**806731**
Stage 2	**−0.026(0.003)**	**0.0493**	**1160530**



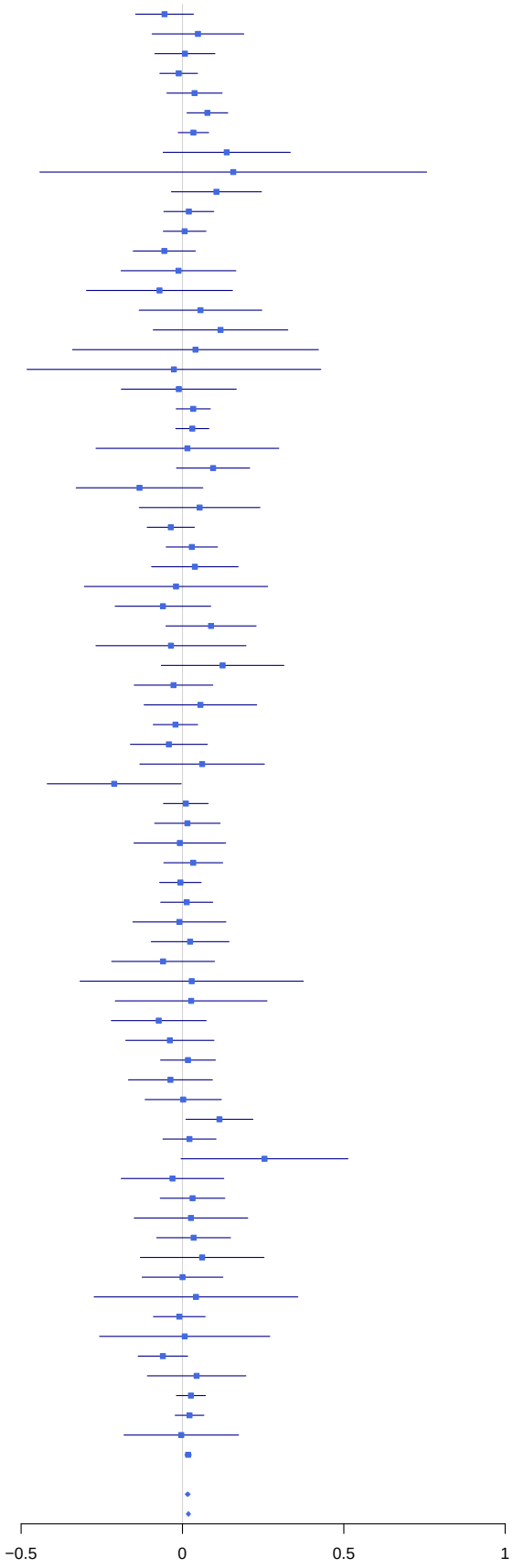
rs17880989, Minor allele/Other allele: A/G (DBP)

Study	Beta(SE)	MAF	N
1958BC	−0.04(0.059)	0.0247	5864
ADDITION	−0.042(0.082)	0.0342	2307
AGES	0.03(0.053)	0.0331	5526
AIRWAVE	0.045(0.04)	0.025	13102
ALSPAC	−0.048(0.071)	0.0157	6529
ARIC	−0.048(0.044)	0.0247	10863
BIOVU	0.05(0.033)	0.0232	19885
BRIGHTcases	−0.131(0.126)	0.0291	1098
BRIGHTcontrols	0.351(0.457)	0.0189	132
CARDIA	−0.086(0.091)	0.0276	2175
CCHS	0.104(0.041)	0.0394	8070
CGPS	0.022(0.035)	0.0372	11783
CHS	0.008(0.073)	0.0226	4109
CIHDS	0.091(0.1)	0.0363	1434
CROATA−KORCULA	0.224(0.268)	0.0086	814
D2D2007	−0.058(0.093)	0.0227	2580
DIABNORD	−0.079(0.102)	0.0521	912
DPS	−0.144(0.205)	0.0276	416
DRSEXTRA	−0.086(0.181)	0.0216	740
EGCUT	−0.021(0.088)	0.0373	1785
EPIC	0.018(0.035)	0.0269	15674
EPIC−Norfolk	0.018(0.033)	0.0263	17850
ERF	0.18(0.185)	0.0126	1153
FamHS	−0.061(0.103)	0.0152	3722
Fenland−CoreExome	−0.252(0.167)	0.0178	1040
Fenland−GWAS	−0.247(0.162)	0.0221	1358
Fenland−OMICS	0.06(0.049)	0.025	8526
FHS	0.064(0.068)	0.0165	7495
FINRISK	0.034(0.073)	0.0189	5153
FINRISK2007	−0.031(0.152)	0.0207	1088
FUSION	0.056(0.072)	0.0231	4237
GAPP	0.384(0.13)	0.0146	1946
GLACIER	−0.019(0.109)	0.0483	922
GoDARTS CAD	−0.077(0.138)	0.0208	1323
GoDARTS	−0.064(0.075)	0.0263	3501
GRAPHIC	0.011(0.107)	0.0257	1887
GS	0.047(0.048)	0.0231	9832
HEALTH	0.024(0.061)	0.0386	3674
HELIC−HA	0.127(0.169)	0.0196	944
HELIC−HP	−0.421(0.216)	0.0204	565
HRS	−0.024(0.047)	0.0248	9621
HUNT	0.099(0.05)	0.0451	4735
INCIPE	−0.087(0.134)	0.0143	1995
INTER99	0.024(0.05)	0.0357	5984
InterAct−CoreExome	0.104(0.039)	0.0311	10915
InterAct−GWAS	0.007(0.06)	0.0255	6675
INV SC	−0.134(0.083)	0.0286	2461
INV UK	0.043(0.078)	0.0256	3242
IPM	−0.022(0.123)	0.025	1342
LBC1921	0.024(0.282)	0.0181	359
LBC1936	−0.027(0.177)	0.0211	783
LIFELINES	0.068(0.094)	0.0305	1948
LRGP	−0.025(0.089)	0.028	2306
MDC	0.049(0.039)	0.0401	8268
MESA	0.104(0.092)	0.0238	2505
METSIM	0.155(0.057)	0.0189	8411
MORGAM	0.126(0.065)	0.0212	5757
NEO	0.082(0.053)	0.0304	6115
NFBC66	0.029(0.132)	0.0214	1353
NFBC86full	−0.146(0.076)	0.0249	3639
OxBB	0.082(0.071)	0.0227	4440
PIVUSULSAM	−0.059(0.078)	0.0423	1998
PPP	0.037(0.062)	0.0285	4766
PROSPER	−0.13(0.126)	0.0251	1275
RS	0.18(0.077)	0.0296	2875
SDC	−0.091(0.156)	0.0452	498
SDR−ANDIS	0.005(0.068)	0.0432	2636
SHIP	0.076(0.053)	0.0258	7160
TwinsUK	0.042(0.154)	0.0327	689
UKHLS	0.044(0.052)	0.0259	7462
VEJLECASES	0.062(0.086)	0.0355	2002
WGHS	0.043(0.032)	0.0233	21964
WHI	−0.007(0.032)	0.0238	21841
WOSCOPS	0.036(0.126)	0.0247	1337
UKBiobank	0.035(0.007)	0.0253	445360
Stage 1	**0.032(0.005)**	**0.0266**	**806731**
Stage 2	**0.032(0.004)**	**0.027**	**1160530**



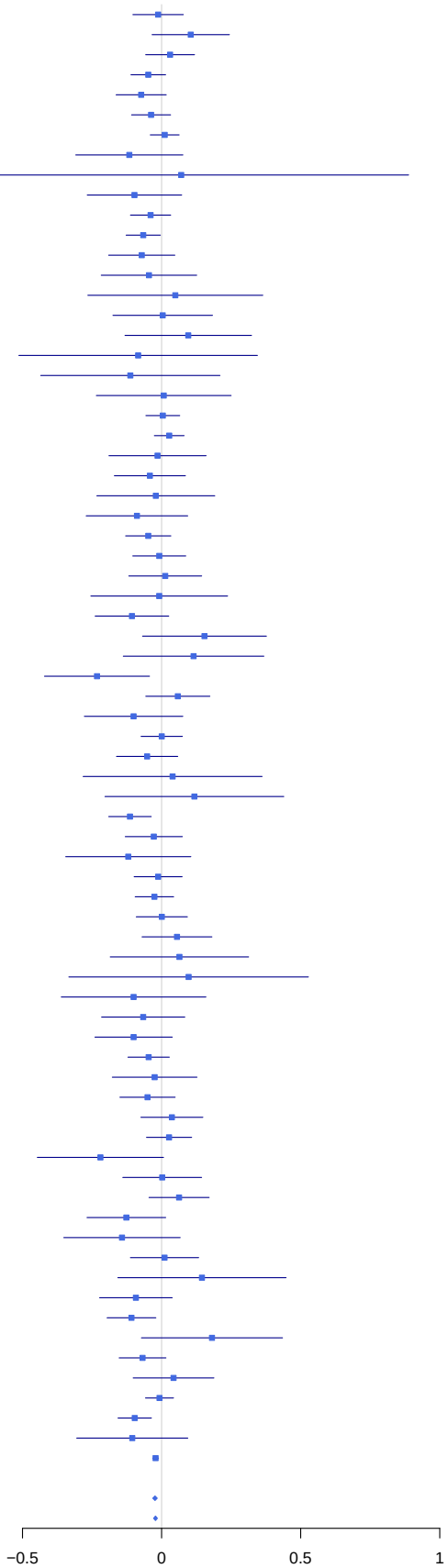
rs33956817, Minor allele/Other allele: C/T (SBP)

Study	Beta(SE)	MAF	N
1958BC	−0.056(0.046)	0.042	5864
ADDITION	0.048(0.072)	0.0433	2307
AGES	0.008(0.047)	0.0413	5526
AIRWAVE	−0.012(0.03)	0.0453	13102
ALSPAC	0.037(0.044)	0.0437	6529
ARIC	0.077(0.032)	0.0475	10864
BIOVU	0.034(0.024)	0.0458	19885
BRIGHTcases	0.137(0.1)	0.0455	1098
BRIGHTcontrols	0.157(0.306)	0.0455	132
CARDIA	0.105(0.071)	0.0467	2175
CCHS	0.02(0.039)	0.0423	8070
CGPS	0.007(0.034)	0.0394	11784
CHS	−0.056(0.049)	0.0515	4113
CIHDS	−0.012(0.091)	0.0432	1436
CROATA−KORCULA	−0.071(0.115)	0.0504	814
D2D2007	0.056(0.097)	0.0213	2580
DIABNORD	0.118(0.106)	0.0504	912
DPS	0.04(0.194)	0.0312	416
DRSEXTRA	−0.027(0.232)	0.0128	740
EGCUT	−0.011(0.091)	0.0353	1785
EPIC	0.033(0.027)	0.0466	15676
EPIC−Norfolk	0.031(0.026)	0.0431	17850
ERF	0.015(0.145)	0.0234	1153
FamHS	0.095(0.058)	0.0493	3722
Fenland−CoreExome	−0.133(0.1)	0.05	1040
Fenland−GWAS	0.053(0.095)	0.0434	1358
Fenland−OMICS	−0.036(0.037)	0.0443	8526
FHS	0.029(0.041)	0.0484	7495
FINRISK	0.038(0.068)	0.0214	5152
FINRISK2007	−0.02(0.145)	0.0221	1088
FUSION	−0.061(0.075)	0.0205	4237
GAPP	0.089(0.071)	0.0574	1947
GLACIER	−0.036(0.119)	0.0369	922
GoDARTS CAD	0.124(0.097)	0.0423	1323
GoDARTS	−0.028(0.062)	0.0388	3501
GRAPHIC	0.056(0.089)	0.0397	1887
GS	−0.022(0.035)	0.0429	9832
HEALTH	−0.042(0.061)	0.038	3674
HELIC−HA	0.061(0.098)	0.0657	944
HELIC−HP	−0.211(0.106)	0.0832	565
HRS	0.01(0.035)	0.044	9621
HUNT	0.015(0.052)	0.0397	4735
INCIPE	−0.008(0.072)	0.0492	1995
INTER99	0.033(0.047)	0.0401	5986
InterAct−CoreExome	−0.006(0.033)	0.045	10915
InterAct−GWAS	0.013(0.041)	0.046	6675
INV SC	−0.01(0.074)	0.0407	2461
INV UK	0.024(0.061)	0.0436	3242
IPM	−0.06(0.081)	0.061	1337
LBC1921	0.029(0.177)	0.046	359
LBC1936	0.027(0.12)	0.046	783
LIFELINES	−0.074(0.075)	0.049	1948
LRGP	−0.039(0.07)	0.0479	2306
MDC	0.017(0.043)	0.0332	8268
MESA	−0.037(0.066)	0.0483	2505
METSIM	0.002(0.06)	0.0166	8411
MORGAM	0.115(0.053)	0.0327	5757
NEO	0.022(0.042)	0.0508	6117
NFBC66	0.254(0.132)	0.0222	1353
NFBC86full	−0.031(0.081)	0.021	3639
OxBB	0.031(0.051)	0.0455	4440
PIVUSULSAM	0.026(0.09)	0.0325	1998
PPP	0.035(0.058)	0.0318	4766
PROSPER	0.061(0.098)	0.0432	1275
RS	0(0.064)	0.0457	2875
SDC	0.042(0.161)	0.0422	498
SHIP	−0.01(0.041)	0.0432	7161
TwinsUK	0.007(0.135)	0.0421	689
UKHLS	−0.061(0.039)	0.0459	7462
VEJLECASES	0.044(0.078)	0.0428	1996
WGHS	0.026(0.023)	0.0453	21964
WHI	0.022(0.023)	0.0464	21841
WOSCOPS	−0.004(0.091)	0.0497	1337
UKBiobank	0.018(0.005)	0.0444	445360
Stage 1	**0.016(0.004)**	**0.0441**	**804099**
Stage 2	**0.018(0.003)**	**0.0443**	**1158190**



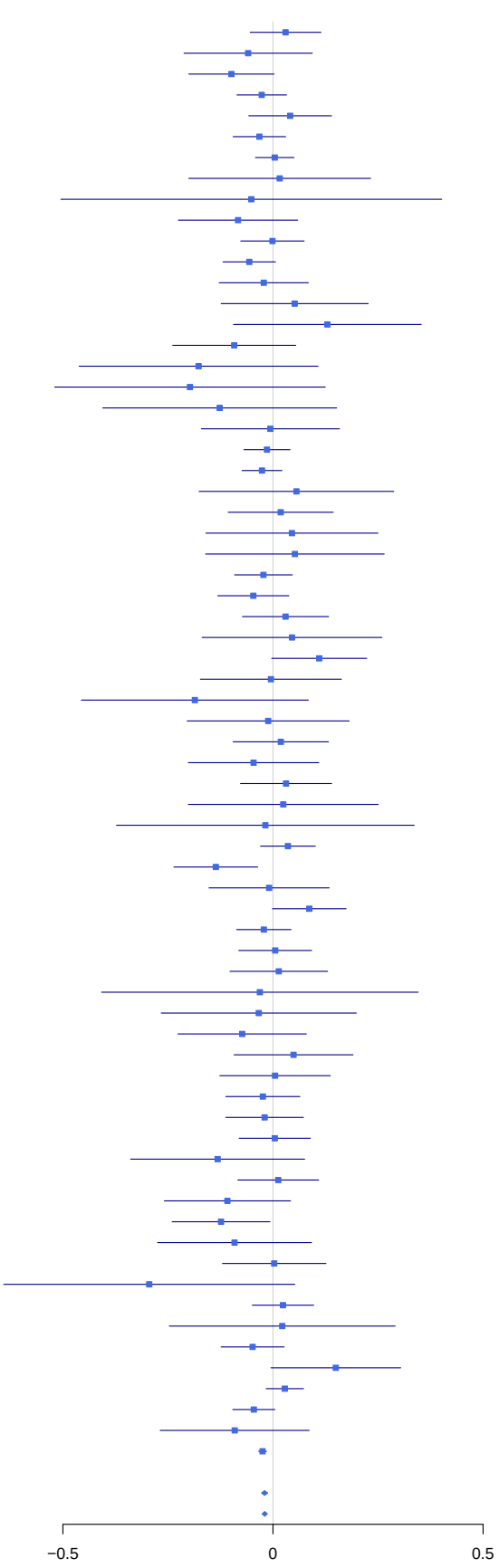
rs34471628, Minor allele/Other allele: G/A (DBP)

Study	Beta(SE)	MAF	N
1958BC	−0.013(0.046)	0.0414	5864
ADDITION	0.105(0.071)	0.0453	2307
AGES	0.031(0.045)	0.0511	5526
AIRWAVE	−0.048(0.032)	0.0388	13102
ALSPAC	−0.073(0.046)	0.0382	6529
ARIC	−0.038(0.036)	0.0373	10863
BIOVU	0.011(0.026)	0.0368	19885
BRIGHTcases	−0.116(0.098)	0.0492	1098
BRIGHTcontrols	0.07(0.417)	0.0227	132
CARDIA	−0.098(0.087)	0.0318	2175
CCHS	−0.04(0.037)	0.0466	8070
CGPS	−0.066(0.031)	0.045	11783
CHS	−0.071(0.061)	0.0342	4109
CIHDS	−0.045(0.088)	0.0471	1434
CROATA−KORCULA	0.049(0.16)	0.0246	814
D2D2007	0.004(0.091)	0.0246	2580
DIABNORD	0.096(0.116)	0.0433	912
DPS	−0.084(0.219)	0.0266	416
DRSEXTRA	−0.112(0.164)	0.0264	740
EGCUT	0.008(0.124)	0.019	1785
EPIC	0.004(0.031)	0.0338	15674
EPIC−Norfolk	0.027(0.027)	0.0395	17850
ERF	−0.015(0.089)	0.0646	1153
FamHS	−0.042(0.065)	0.0372	3722
Fenland−CoreExome	−0.021(0.108)	0.0428	1040
Fenland−GWAS	−0.089(0.093)	0.0466	1358
Fenland−OMICS	−0.048(0.041)	0.0357	8526
FHS	−0.008(0.049)	0.0339	7495
FINRISK	0.013(0.067)	0.0225	5153
FINRISK2007	−0.009(0.125)	0.0271	1088
FUSION	−0.107(0.067)	0.0268	4237
GAPP	0.154(0.114)	0.02	1946
GLACIER	0.115(0.129)	0.0325	922
GoDARTS CAD	−0.232(0.096)	0.0438	1323
GoDARTS	0.058(0.059)	0.0437	3501
GRAPHIC	−0.101(0.09)	0.0368	1887
GS	0.001(0.038)	0.0383	9832
HEALTH	−0.052(0.056)	0.0452	3674
HELIC−HA	0.04(0.164)	0.0196	944
HELIC−HP	0.118(0.164)	0.0363	565
HRS	−0.114(0.039)	0.0357	9621
HUNT	−0.028(0.052)	0.0395	4735
INCIPE	−0.12(0.115)	0.0198	1995
INTER99	−0.012(0.044)	0.0454	5984
InterAct−CoreExome	−0.026(0.035)	0.0378	10915
InterAct−GWAS	0.001(0.047)	0.0363	6675
INV UK	0.055(0.064)	0.0398	3242
IPM	0.064(0.127)	0.0228	1342
LBC1921	0.097(0.22)	0.0306	359
LBC1936	−0.101(0.133)	0.0377	783
LIFELINES	−0.066(0.076)	0.0475	1948
LRGP	−0.101(0.071)	0.0444	2306
MDC	−0.047(0.038)	0.0441	8268
MESA	−0.025(0.078)	0.0339	2505
METSIM	−0.051(0.051)	0.0249	8411
MORGAM	0.037(0.057)	0.0273	5757
NEO	0.027(0.041)	0.0514	6115
NFBC66	−0.22(0.116)	0.0285	1353
NFBC86full	0.002(0.072)	0.027	3639
OxBB	0.063(0.055)	0.0386	4440
PIVUSULSAM	−0.127(0.072)	0.0526	1998
PROSPER	−0.142(0.107)	0.0353	1275
RS	0.011(0.063)	0.0463	2875
SDC	0.145(0.154)	0.0462	498
SDR−ANDIS	−0.092(0.067)	0.044	2636
SHIP	−0.108(0.045)	0.0366	7160
TwinsUK	0.181(0.129)	0.0443	689
UKHLS	−0.068(0.043)	0.0381	7462
VEJLECASES	0.043(0.074)	0.0482	2002
WGHS	−0.008(0.026)	0.0355	21964
WHI	−0.097(0.031)	0.0332	21841
WOSCOPS	−0.105(0.102)	0.0381	1337
UKBiobank	−0.022(0.005)	0.0392	445360
Stage 1	**−0.024(0.004)**	**0.0389**	**799504**
Stage 2	**−0.022(0.003)**	**0.0392**	**1153300**



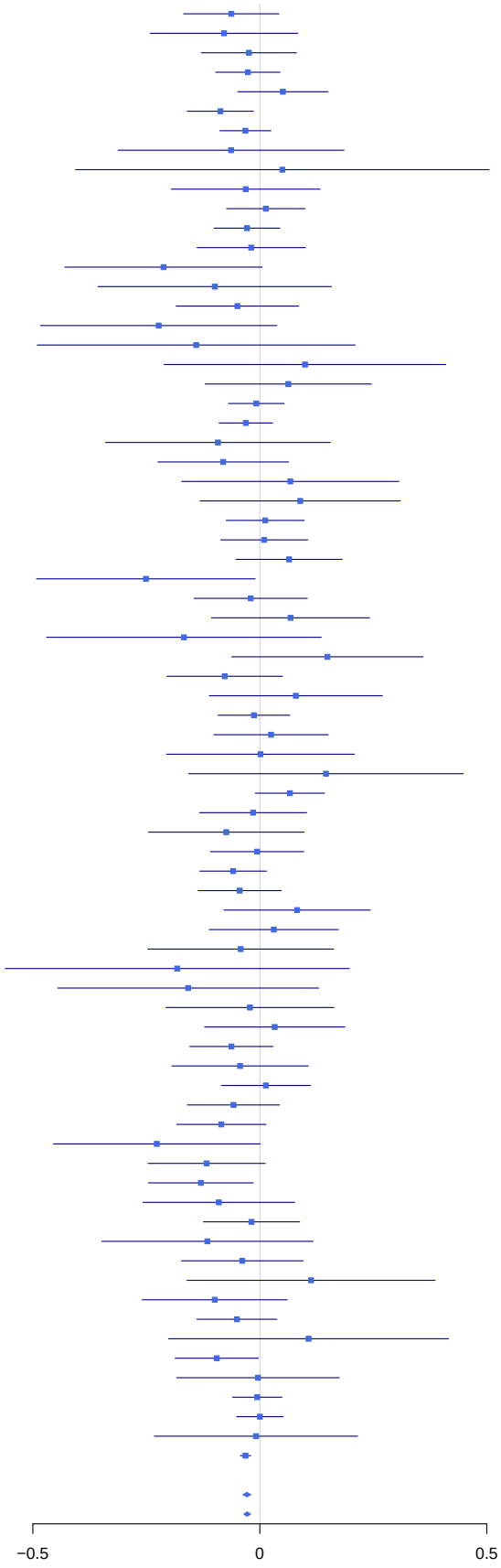
rs34674752, Minor allele/Other allele: A/G (DBP)

Study	Beta(SE)	MAF	N
1958BC	0.03(0.043)	0.0516	5864
ADDITION	−0.059(0.078)	0.0366	2307
AGES	−0.099(0.052)	0.0359	5526
AIRWAVE	−0.027(0.03)	0.0511	13102
ALSPAC	0.041(0.05)	0.0344	6529
ARIC	−0.032(0.032)	0.0476	10863
BIOVU	0.004(0.023)	0.0503	19885
BRIGHTcases	0.016(0.11)	0.0396	1098
BRIGHTcontrols	−0.052(0.231)	0.0682	132
CARDIA	−0.083(0.072)	0.0474	2175
CCHS	−0.001(0.039)	0.0447	8070
CGPS	−0.056(0.032)	0.0451	11783
CHS	−0.022(0.054)	0.0436	4109
CIHDS	0.052(0.089)	0.0432	1434
CROATA−KORCULA	0.129(0.114)	0.0499	814
D2D2007	−0.092(0.075)	0.0372	2580
DIABNORD	−0.177(0.145)	0.0263	912
DPS	−0.198(0.164)	0.0493	416
DRSEXTRA	−0.127(0.142)	0.0345	740
EGCUT	−0.006(0.084)	0.0409	1785
EPIC	−0.014(0.028)	0.0435	15674
EPIC−Norfolk	−0.026(0.024)	0.0501	17850
ERF	0.056(0.118)	0.0317	1153
FamHS	0.018(0.064)	0.0389	3722
Fenland−CoreExome	0.045(0.104)	0.0476	1040
Fenland−GWAS	0.052(0.108)	0.0551	1358
Fenland−OMICS	−0.023(0.035)	0.0496	8526
FHS	−0.047(0.043)	0.0443	7495
FINRISK	0.03(0.052)	0.0365	5153
FINRISK2007	0.045(0.109)	0.04	1088
FUSION	0.11(0.058)	0.0376	4237
GAPP	−0.005(0.086)	0.036	1946
GLACIER	−0.186(0.138)	0.0304	922
GoDARTS CAD	−0.011(0.098)	0.0427	1323
GoDARTS	0.019(0.058)	0.0447	3501
GRAPHIC	−0.046(0.079)	0.0527	1887
HEALTH	0.031(0.055)	0.0456	3674
HELIC−HA	0.024(0.115)	0.0413	944
HELIC−HP	−0.018(0.181)	0.0257	565
HRS	0.036(0.033)	0.0483	9621
HUNT	−0.136(0.051)	0.0431	4735
INCIPE	−0.009(0.073)	0.0481	1995
INTER99	0.086(0.045)	0.0446	5984
InterAct−CoreExome	−0.022(0.033)	0.0439	10915
InterAct−GWAS	0.005(0.044)	0.0467	6675
INV UK	0.014(0.059)	0.0475	3242
LBC1921	−0.031(0.192)	0.0376	359
LBC1936	−0.034(0.118)	0.0492	783
LIFELINES	−0.073(0.078)	0.0431	1948
LRGP	0.049(0.072)	0.0438	2306
MESA	0.005(0.067)	0.0457	2505
METSIM	−0.024(0.045)	0.0322	8411
MORGAM	−0.02(0.047)	0.0412	5757
NEO	0.004(0.043)	0.0482	6115
NFBC66	−0.132(0.106)	0.0347	1353
OxBB	0.012(0.049)	0.0476	4440
PIVUSULSAM	−0.109(0.077)	0.0448	1998
PPP	−0.124(0.059)	0.0306	4766
PROSPER	−0.092(0.093)	0.0478	1275
RS	0.003(0.063)	0.0463	2875
SDC	−0.295(0.177)	0.0321	498
SHIP	0.024(0.037)	0.0561	7160
TwinsUK	0.022(0.137)	0.0421	689
UKHLS	−0.048(0.038)	0.0495	7462
VEJLECASES	0.149(0.079)	0.0417	2002
WGHS	0.028(0.023)	0.0475	21964
WHI	−0.046(0.026)	0.0477	21841
WOSCOPS	−0.091(0.09)	0.049	1337
UKBiobank	−0.025(0.005)	0.0508	445360
Stage 1	**−0.02(0.004)**	**0.0489**	**778553**
Stage 2	**−0.02(0.003)**	**0.0485**	**1132350**



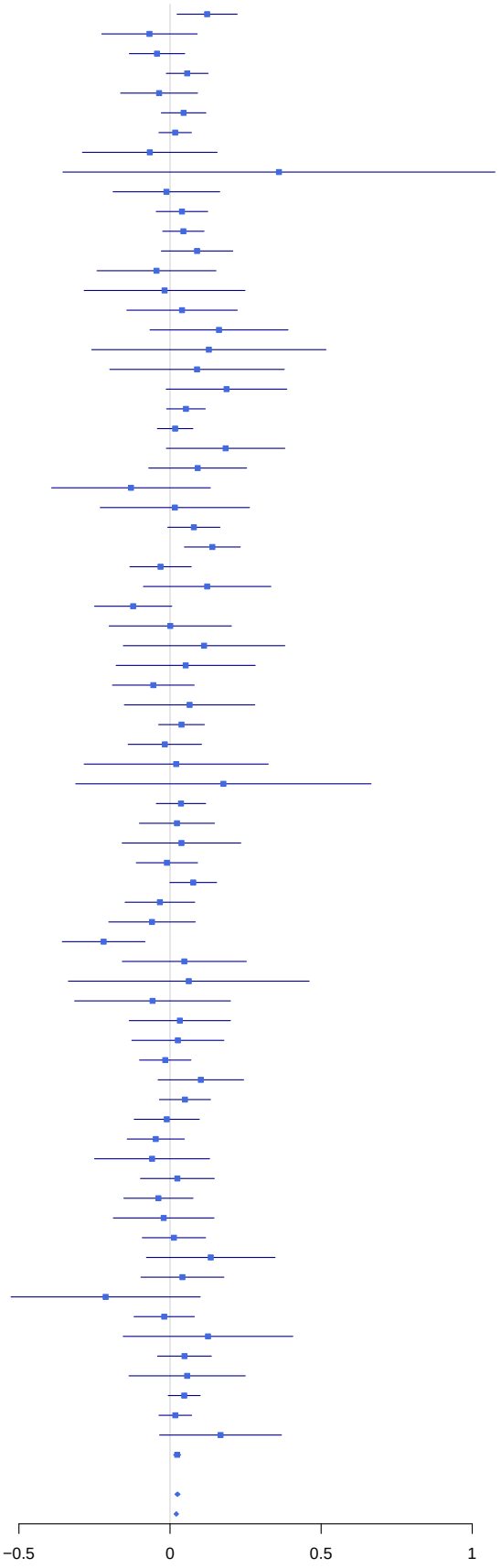
rs3821033, Minor allele/Other allele: T/C (DBP)

Study	Beta(SE)	MAF	N
1958BC	−0.063(0.054)	0.0321	5864
ADDITION	−0.079(0.083)	0.034	2307
AGES	−0.024(0.053)	0.034	5526
AIRWAVE	−0.026(0.036)	0.0323	13102
ALSPAC	0.051(0.051)	0.0326	6529
ARIC	−0.087(0.037)	0.0366	10863
BIOVU	−0.032(0.029)	0.0321	19885
BRIGHTcases	−0.063(0.127)	0.0278	1098
BRIGHTcontrols	0.05(0.232)	0.0758	132
CARDIA	−0.031(0.084)	0.0338	2175
CCHS	0.013(0.044)	0.0338	8070
CGPS	−0.028(0.037)	0.0334	11783
CHS	−0.019(0.061)	0.0351	4109
CIHDS	−0.212(0.111)	0.0293	1434
CROATA−KORCULA	−0.099(0.131)	0.0332	814
D2D2007	−0.049(0.069)	0.0444	2580
DIABNORD	−0.223(0.133)	0.0307	912
DPS	−0.14(0.179)	0.0409	416
DRSEXTRA	0.099(0.158)	0.027	740
EGCUT	0.063(0.093)	0.0325	1785
EPIC	−0.008(0.031)	0.0344	15674
EPIC−Norfolk	−0.031(0.03)	0.0317	17850
ERF	−0.092(0.126)	0.0299	1153
FamHS	−0.081(0.073)	0.0289	3722
Fenland−CoreExome	0.067(0.122)	0.0346	1040
Fenland−GWAS	0.089(0.113)	0.0302	1358
Fenland−OMICS	0.012(0.044)	0.0324	8526
FHS	0.01(0.049)	0.0336	7495
FINRISK	0.065(0.06)	0.0286	5153
FINRISK2007	−0.251(0.123)	0.0326	1088
FUSION	−0.02(0.064)	0.0312	4237
GAPP	0.068(0.089)	0.0342	1946
GLACIER	−0.167(0.154)	0.0239	922
GoDARTS CAD	0.149(0.108)	0.0325	1323
GoDARTS	−0.077(0.065)	0.0346	3501
GRAPHIC	0.079(0.097)	0.0342	1887
GS	−0.013(0.04)	0.0354	9832
HEALTH	0.025(0.064)	0.0351	3674
HELIC−HA	0.001(0.106)	0.0471	944
HELIC−HP	0.146(0.154)	0.0336	565
HRS	0.066(0.039)	0.0361	9621
HUNT	−0.015(0.06)	0.0297	4735
INCIPE	−0.074(0.087)	0.0341	1995
INTER99	−0.006(0.053)	0.0333	5984
InterAct−CoreExome	−0.059(0.037)	0.0339	10915
InterAct−GWAS	−0.045(0.047)	0.035	6675
INV SC	0.082(0.082)	0.0311	2461
INV UK	0.031(0.073)	0.0308	3242
IPM	−0.042(0.104)	0.0361	1342
LBC1921	−0.182(0.193)	0.0404	359
LBC1936	−0.158(0.147)	0.0307	783
LIFELINES	−0.022(0.094)	0.0295	1948
LRGP	0.033(0.079)	0.0373	2306
MDC	−0.063(0.047)	0.0288	8268
MESA	−0.044(0.077)	0.0341	2505
METSIM	0.013(0.05)	0.0267	8411
MORGAM	−0.058(0.052)	0.0336	5757
NEO	−0.085(0.05)	0.0337	6115
NFBC66	−0.227(0.116)	0.0273	1353
NFBC86full	−0.117(0.066)	0.0326	3639
OxBB	−0.13(0.059)	0.0336	4440
PIVUSULSAM	−0.09(0.085)	0.0348	1998
PPP	−0.018(0.054)	0.0394	4766
PROSPER	−0.116(0.119)	0.0286	1275
RS	−0.039(0.068)	0.0384	2875
SDC	0.113(0.139)	0.0512	498
SDR−ANDIS	−0.099(0.082)	0.0286	2636
SHIP	−0.05(0.045)	0.0377	7160
TwinsUK	0.107(0.157)	0.0312	689
UKHLS	−0.095(0.047)	0.0321	7462
VEJLECASES	−0.004(0.091)	0.032	2002
WGHS	−0.006(0.028)	0.0338	21964
WHI	0(0.026)	0.0354	21841
WOSCOPS	−0.009(0.114)	0.0299	1337
UKBiobank	−0.032(0.006)	0.0326	445360
Stage 1	**−0.029(0.004)**	**0.033**	**806731**
Stage 2	**−0.028(0.004)**	**0.0331**	**1160530**



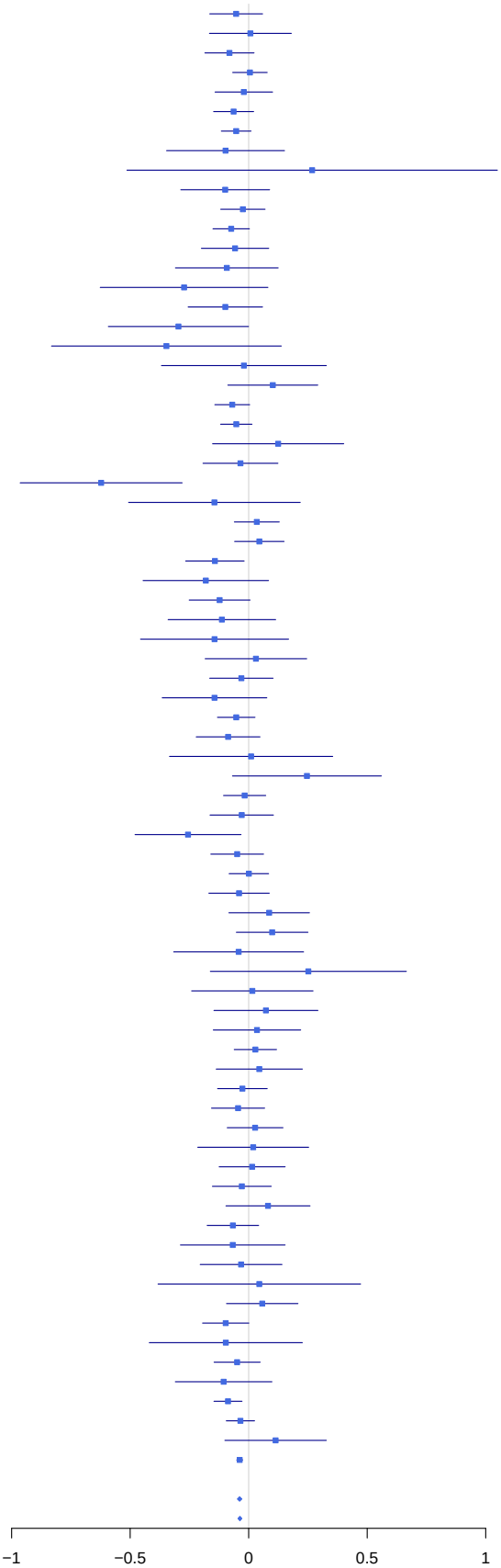
rs4149909, Minor allele/Other allele: G/A (SBP)

Study	Beta(SE)	MAF	N
1958BC	0.123(0.051)	0.0346	5864
ADDITION	−0.068(0.081)	0.0355	2307
AGES	−0.043(0.047)	0.0434	5526
AIRWAVE	0.057(0.035)	0.0314	13102
ALSPAC	−0.036(0.065)	0.0196	6529
ARIC	0.045(0.038)	0.0327	10864
BIOVU	0.017(0.027)	0.0344	19885
BRIGHTcases	−0.067(0.114)	0.036	1098
BRIGHTcontrols	0.36(0.365)	0.0303	132
CARDIA	−0.012(0.09)	0.0301	2175
CCHS	0.04(0.043)	0.0346	8070
CGPS	0.044(0.035)	0.0367	11784
CHS	0.09(0.06)	0.0349	4113
CIHDS	−0.045(0.1)	0.0373	1436
CROATA−KORCULA	−0.018(0.136)	0.0369	814
D2D2007	0.04(0.093)	0.0231	2580
DIABNORD	0.162(0.117)	0.0417	912
DPS	0.128(0.198)	0.03	416
DRSEXTRA	0.089(0.147)	0.0318	740
EGCUT	0.187(0.102)	0.028	1785
EPIC	0.053(0.033)	0.0304	15676
EPIC−Norfolk	0.017(0.03)	0.0322	17850
ERF	0.184(0.1)	0.0481	1153
FamHS	0.092(0.083)	0.023	3722
Fenland−CoreExome	−0.129(0.134)	0.0284	1040
Fenland−GWAS	0.016(0.126)	0.0318	1358
Fenland−OMICS	0.079(0.044)	0.0309	8526
FHS	0.14(0.047)	0.0359	7495
FINRISK	−0.031(0.052)	0.0377	5152
FINRISK2007	0.123(0.108)	0.0418	1088
FUSION	−0.122(0.065)	0.0291	4237
GAPP	0.001(0.103)	0.0241	1947
GLACIER	0.113(0.136)	0.0298	922
GoDARTS CAD	0.052(0.117)	0.0295	1323
GoDARTS	−0.055(0.069)	0.0317	3501
GRAPHIC	0.065(0.11)	0.0241	1887
GS	0.038(0.039)	0.0353	9832
HEALTH	−0.017(0.062)	0.0365	3674
HELIC−HA	0.02(0.155)	0.0238	944
HELIC−HP	0.177(0.249)	0.015	565
HRS	0.036(0.042)	0.0307	9621
HUNT	0.023(0.063)	0.0273	4735
INCIPE	0.038(0.1)	0.0258	1995
INTER99	−0.01(0.052)	0.0334	5986
InterAct−CoreExome	0.077(0.039)	0.0304	10915
InterAct−GWAS	−0.033(0.059)	0.0295	6675
INV SC	−0.06(0.073)	0.0411	2461
INV UK	−0.22(0.07)	0.0329	3242
IPM	0.047(0.105)	0.036	1337
LBC1921	0.062(0.203)	0.0362	359
LBC1936	−0.058(0.132)	0.037	783
LIFELINES	0.033(0.085)	0.0357	1948
LRGP	0.026(0.078)	0.0379	2306
MDC	−0.016(0.043)	0.0332	8268
MESA	0.102(0.072)	0.0399	2505
METSIM	0.049(0.043)	0.0339	8411
MORGAM	−0.011(0.055)	0.0295	5757
NEO	−0.047(0.048)	0.0361	6117
NFBC66	−0.059(0.097)	0.041	1353
NFBC86full	0.024(0.062)	0.0377	3639
OxBB	−0.038(0.058)	0.034	4440
PIVUSULSAM	−0.021(0.085)	0.035	1998
PPP	0.013(0.053)	0.0392	4766
PROSPER	0.135(0.109)	0.0349	1275
RS	0.041(0.07)	0.0372	2875
SDC	−0.213(0.16)	0.0382	498
SHIP	−0.019(0.051)	0.0282	7161
TwinsUK	0.126(0.143)	0.0348	689
UKHLS	0.048(0.045)	0.0331	7462
VEJLECASES	0.057(0.098)	0.0278	1996
WGHS	0.047(0.027)	0.0319	21964
WHI	0.017(0.028)	0.031	21841
WOSCOPS	0.167(0.103)	0.0374	1337
UKBiobank	0.024(0.006)	0.0327	445360
Stage 1	**0.025(0.004)**	**0.0329**	**804099**
Stage 2	**0.021(0.004)**	**0.0333**	**1158190**



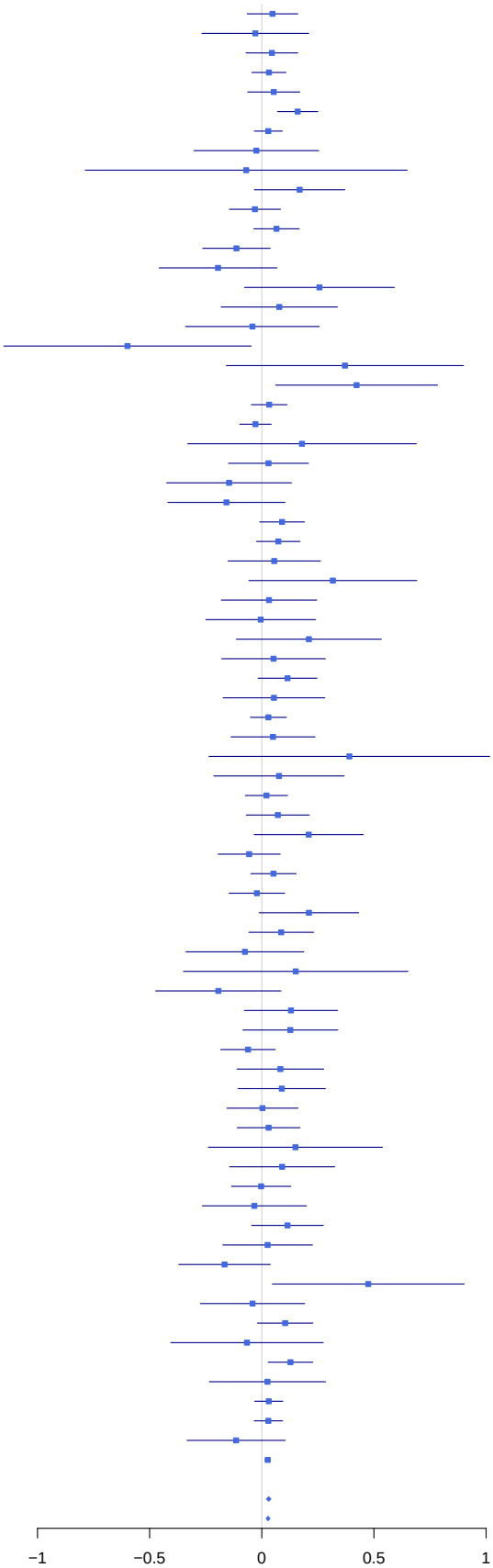
rs45573936, Minor allele/Other allele: C/T (DBP)

Study	Beta(SE)	MAF	N
1958BC	−0.053(0.057)	0.0275	5864
ADDITION	0.007(0.088)	0.0284	2307
AGES	−0.081(0.053)	0.0343	5526
AIRWAVE	0.005(0.037)	0.0285	13102
ALSPAC	−0.021(0.062)	0.0208	6529
ARIC	−0.064(0.043)	0.0252	10863
BIOVU	−0.053(0.032)	0.0249	19885
BRIGHTcases	−0.098(0.127)	0.0278	1098
BRIGHTcontrols	0.268(0.399)	0.0265	132
CARDIA	−0.099(0.096)	0.0255	2175
CCHS	−0.024(0.048)	0.0279	8070
CGPS	−0.074(0.039)	0.0281	11783
CHS	−0.057(0.072)	0.0232	4109
CIHDS	−0.092(0.111)	0.0303	1434
CROATA−KORCULA	−0.272(0.18)	0.019	814
D2D2007	−0.099(0.08)	0.0306	2580
DIABNORD	−0.296(0.151)	0.0241	912
DPS	−0.347(0.247)	0.0204	416
DRSEXTRA	−0.02(0.177)	0.0209	740
EGCUT	0.102(0.097)	0.0319	1785
EPIC	−0.069(0.038)	0.0227	15674
EPIC−Norfolk	−0.052(0.034)	0.025	17850
ERF	0.124(0.141)	0.0234	1153
FamHS	−0.035(0.081)	0.026	3722
Fenland−CoreExome	−0.622(0.174)	0.0163	1040
Fenland−GWAS	−0.145(0.185)	0.0162	1358
Fenland−OMICS	0.034(0.048)	0.0255	8526
FHS	0.045(0.053)	0.0279	7495
FINRISK	−0.142(0.063)	0.0253	5153
FINRISK2007	−0.181(0.135)	0.0267	1088
FUSION	−0.123(0.066)	0.0282	4237
GAPP	−0.113(0.116)	0.0194	1946
GLACIER	−0.144(0.159)	0.0211	922
GoDARTS CAD	0.031(0.109)	0.0314	1323
GoDARTS	−0.031(0.068)	0.0313	3501
GRAPHIC	−0.144(0.113)	0.0239	1887
GS	−0.052(0.04)	0.0325	9832
HEALTH	−0.087(0.069)	0.0299	3674
HELIC−HA	0.01(0.176)	0.018	944
HELIC−HP	0.246(0.16)	0.0363	565
HRS	−0.017(0.045)	0.0259	9621
HUNT	−0.029(0.068)	0.0233	4735
INCIPE	−0.256(0.114)	0.0201	1995
INTER99	−0.049(0.057)	0.0273	5984
InterAct−CoreExome	0.001(0.043)	0.0258	10915
InterAct−GWAS	−0.041(0.065)	0.0211	6675
INV SC	0.086(0.087)	0.0287	2461
INV UK	0.099(0.077)	0.0261	3242
IPM	−0.042(0.14)	0.0201	1342
LBC1921	0.252(0.211)	0.0334	359
LBC1936	0.015(0.131)	0.0377	783
LIFELINES	0.073(0.112)	0.0208	1948
LRGP	0.035(0.094)	0.0254	2306
MDC	0.028(0.046)	0.03	8268
MESA	0.045(0.093)	0.0232	2505
METSIM	−0.026(0.053)	0.0215	8411
MORGAM	−0.045(0.057)	0.0266	5757
NEO	0.027(0.06)	0.023	6115
NFBC66	0.019(0.119)	0.0266	1353
NFBC86full	0.015(0.071)	0.028	3639
OxBB	−0.029(0.063)	0.0291	4440
PIVUSULSAM	0.081(0.09)	0.0315	1998
PPP	−0.067(0.055)	0.0343	4766
PROSPER	−0.067(0.113)	0.0322	1275
RS	−0.032(0.088)	0.0228	2875
SDC	0.045(0.218)	0.0221	498
SDR−ANDIS	0.057(0.077)	0.0336	2636
SHIP	−0.097(0.05)	0.0288	7160
TwinsUK	−0.096(0.165)	0.0283	689
UKHLS	−0.049(0.05)	0.0281	7462
VEJLECASES	−0.106(0.104)	0.0237	2002
WGHS	−0.087(0.03)	0.0255	21964
WHI	−0.035(0.03)	0.0252	21841
WOSCOPS	0.114(0.109)	0.0318	1337
UKBiobank	−0.038(0.006)	0.0275	445360
Stage 1	**−0.038(0.005)**	**0.0271**	**806731**
Stage 2	**−0.037(0.004)**	**0.027**	**1160530**



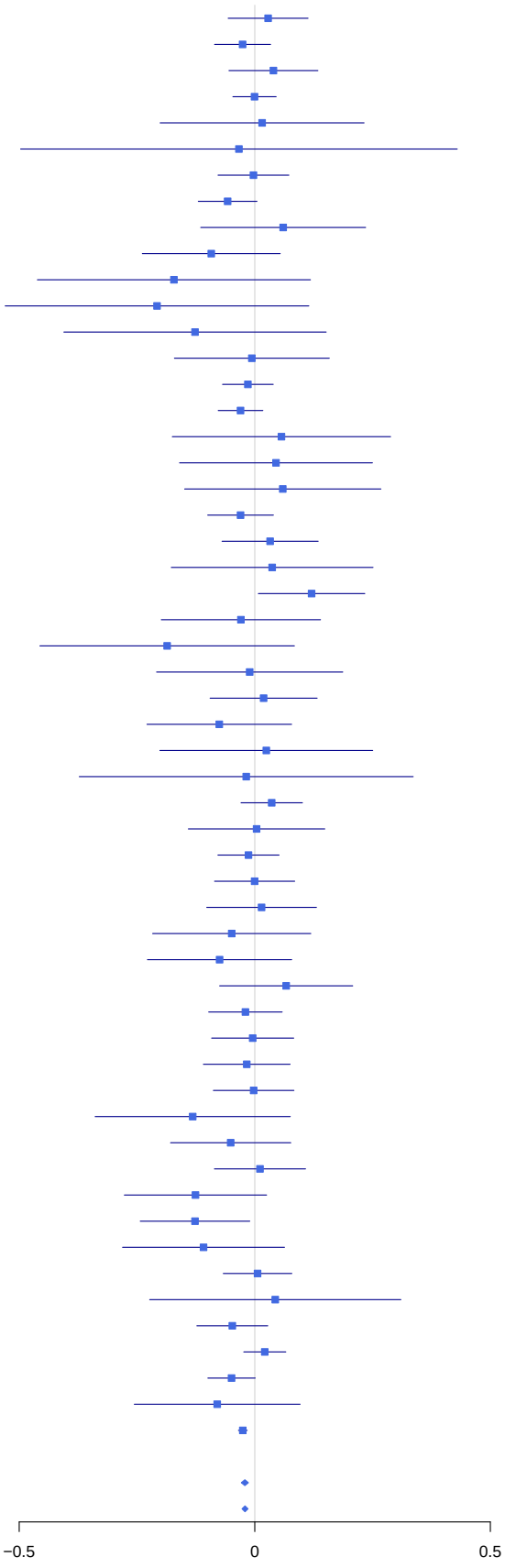
rs56335308, Minor allele/Other allele: A/G (DBP)

Study	Beta(SE)	MAF	N
1958BC	0.048(0.058)	0.0259	5864
ADDITION	−0.029(0.122)	0.0147	2307
AGES	0.045(0.059)	0.0276	5526
AIRWAVE	0.032(0.039)	0.0261	13102
ALSPAC	0.053(0.059)	0.023	6529
ARIC	0.16(0.046)	0.0224	10863
BIOVU	0.029(0.032)	0.0255	19885
BRIGHTcases	−0.024(0.142)	0.0237	1098
BRIGHTcontrols	−0.07(0.366)	0.0303	132
CARDIA	0.169(0.103)	0.0228	2175
CCHS	−0.031(0.058)	0.0185	8070
CGPS	0.066(0.052)	0.0163	11783
CHS	−0.113(0.077)	0.0212	4109
CIHDS	−0.195(0.134)	0.0202	1434
CROATA−KORCULA	0.257(0.17)	0.0209	814
D2D2007	0.078(0.132)	0.0114	2580
DIABNORD	−0.042(0.152)	0.0225	912
DPS	−0.599(0.281)	0.0156	416
DRSEXTRA	0.37(0.27)	0.0095	740
EGCUT	0.423(0.184)	0.0084	1785
EPIC	0.033(0.041)	0.0195	15674
EPIC−Norfolk	−0.028(0.036)	0.0224	17850
ERF	0.179(0.26)	0.0069	1153
FamHS	0.03(0.091)	0.0192	3722
Fenland−CoreExome	−0.146(0.142)	0.024	1040
Fenland−GWAS	−0.158(0.133)	0.022	1358
Fenland−OMICS	0.09(0.051)	0.0232	8526
FHS	0.074(0.05)	0.0335	7495
FINRISK	0.055(0.105)	0.0087	5153
FINRISK2007	0.317(0.191)	0.0119	1088
FUSION	0.032(0.109)	0.0103	4237
GAPP	−0.005(0.125)	0.017	1946
GLACIER	0.21(0.165)	0.0184	922
GoDARTS CAD	0.052(0.118)	0.0272	1323
GoDARTS	0.115(0.067)	0.0324	3501
GRAPHIC	0.054(0.116)	0.0223	1887
GS	0.029(0.041)	0.0312	9832
HEALTH	0.05(0.096)	0.0151	3674
HELIC−HA	0.39(0.319)	0.0053	944
HELIC−HP	0.077(0.148)	0.0407	565
HRS	0.021(0.048)	0.0232	9621
HUNT	0.071(0.072)	0.021	4735
INCIPE	0.209(0.124)	0.0168	1995
INTER99	−0.056(0.071)	0.0173	5984
InterAct−CoreExome	0.052(0.051)	0.0178	10915
InterAct−GWAS	−0.022(0.063)	0.0205	6675
INV SC	0.21(0.113)	0.0165	2461
INV UK	0.087(0.074)	0.0299	3242
IPM	−0.075(0.134)	0.0209	1342
LBC1921	0.151(0.255)	0.0223	359
LBC1936	−0.194(0.143)	0.0319	783
LIFELINES	0.13(0.106)	0.0228	1948
LRGP	0.127(0.108)	0.0189	2306
MDC	−0.061(0.062)	0.0153	8268
MESA	0.083(0.098)	0.0198	2505
METSIM	0.089(0.099)	0.0061	8411
MORGAM	0.003(0.081)	0.0131	5757
NEO	0.03(0.071)	0.0164	6115
NFBC66	0.15(0.198)	0.0096	1353
NFBC86full	0.091(0.12)	0.0098	3639
OxBB	−0.003(0.068)	0.0256	4440
PIVUSULSAM	−0.033(0.118)	0.018	1998
PPP	0.115(0.082)	0.0159	4766
PROSPER	0.026(0.102)	0.0365	1275
RS	−0.166(0.104)	0.0162	2875
SDC	0.475(0.218)	0.0221	498
SDR−ANDIS	−0.041(0.119)	0.0138	2636
SHIP	0.104(0.063)	0.0174	7160
TwinsUK	−0.066(0.173)	0.0254	689
UKHLS	0.128(0.051)	0.0266	7462
VEJLECASES	0.025(0.132)	0.0147	2002
WGHS	0.031(0.032)	0.0228	21964
WHI	0.029(0.032)	0.0226	21841
WOSCOPS	−0.114(0.112)	0.031	1337
UKBiobank	0.026(0.006)	0.0271	445360
Stage 1	**0.031(0.005)**	**0.0253**	**806731**
Stage 2	**0.028(0.004)**	**0.0248**	**1160530**



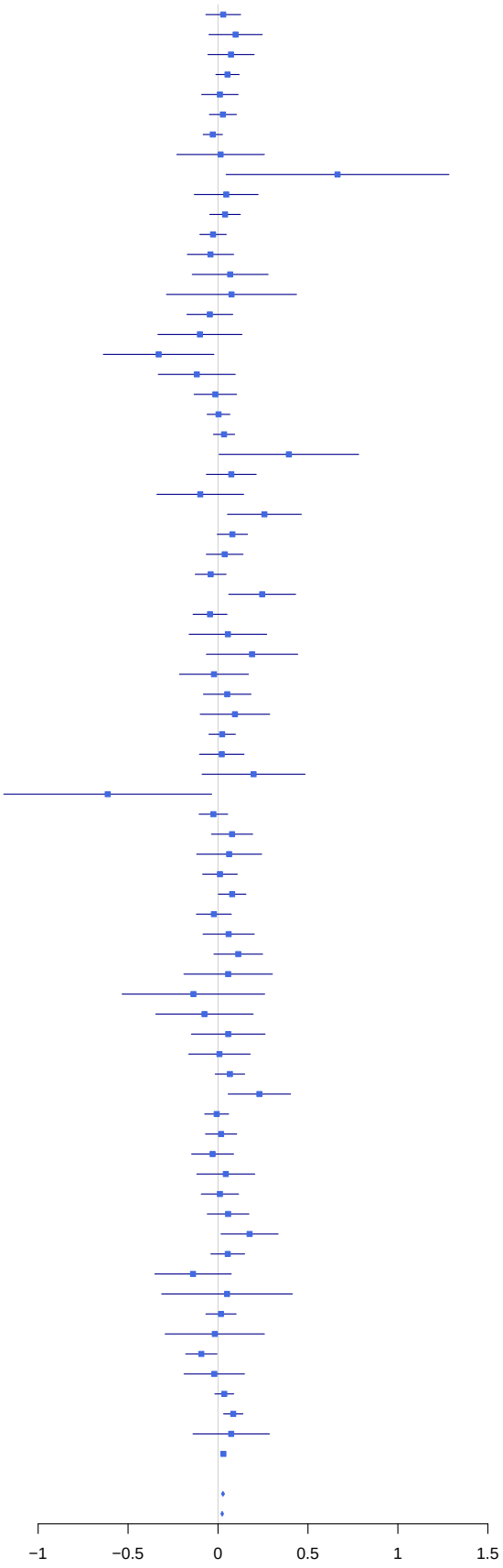
rs61732533, Minor allele/Other allele: A/G (DBP)

Study	Beta(SE)	MAF	N
1958BC	0.028(0.043)	0.051	5864
AIRWAVE	−0.026(0.03)	0.0504	13102
ALSPAC	0.04(0.048)	0.037	6529
BIOVU	−0.001(0.023)	0.0499	19885
BRIGHTcases	0.016(0.11)	0.0397	1098
BRIGHTcontrols	−0.034(0.236)	0.0644	132
CCHS	−0.003(0.038)	0.0447	8070
CGPS	−0.058(0.032)	0.0451	11783
CIHDS	0.06(0.089)	0.0432	1434
D2D2007	−0.092(0.075)	0.0372	2580
DIABNORD	−0.172(0.148)	0.0252	912
DPS	−0.207(0.164)	0.0502	416
DRSEXTRA	−0.127(0.142)	0.0345	740
EGCUT	−0.006(0.084)	0.0409	1785
EPIC	−0.015(0.027)	0.0434	15674
EPIC−Norfolk	−0.03(0.024)	0.0502	17850
ERF	0.057(0.118)	0.0317	1153
Fenland−CoreExome	0.045(0.104)	0.0476	1040
Fenland−GWAS	0.059(0.106)	0.056	1358
Fenland−OMICS	−0.03(0.036)	0.0492	8526
FINRISK	0.033(0.052)	0.0367	5153
FINRISK2007	0.037(0.109)	0.04	1088
FUSION	0.121(0.058)	0.0375	4237
GAPP	−0.029(0.086)	0.0355	1946
GLACIER	−0.186(0.138)	0.0304	922
GoDARTS CAD	−0.011(0.101)	0.0406	1323
GoDARTS	0.019(0.058)	0.0448	3501
GRAPHIC	−0.075(0.078)	0.0549	1887
HELIC−HA	0.024(0.115)	0.0413	944
HELIC−HP	−0.018(0.181)	0.0257	565
HRS	0.036(0.033)	0.0482	9621
INCIPE	0.004(0.074)	0.0474	1995
InterAct−CoreExome	−0.013(0.033)	0.0436	10915
InterAct−GWAS	0(0.043)	0.0471	6675
INV UK	0.014(0.059)	0.0472	3242
IPM	−0.049(0.086)	0.0538	1342
LIFELINES	−0.075(0.078)	0.0429	1948
LRGP	0.067(0.072)	0.044	2306
MDC	−0.02(0.04)	0.0426	8268
METSIM	−0.004(0.044)	0.0346	8411
MORGAM	−0.017(0.047)	0.0413	5757
NEO	−0.002(0.044)	0.0475	6115
NFBC66	−0.132(0.106)	0.0347	1353
NFBC86full	−0.051(0.065)	0.0336	3639
OxBB	0.011(0.049)	0.0471	4440
PIVUSULSAM	−0.126(0.077)	0.0449	1998
PPP	−0.127(0.059)	0.0307	4766
PROSPER	−0.109(0.088)	0.0487	1275
SHIP	0.006(0.037)	0.0585	7160
TwinsUK	0.043(0.136)	0.0428	689
UKHLS	−0.048(0.038)	0.0491	7462
WGHS	0.021(0.023)	0.0472	21964
WHI	−0.049(0.026)	0.0477	21841
WOSCOPS	−0.08(0.09)	0.049	1337
UKBiobank	−0.025(0.005)	0.0503	445360
Stage 1	**−0.021(0.004)**	**0.0489**	**731376**
Stage 2	**−0.021(0.003)**	**0.0484**	**1085170**



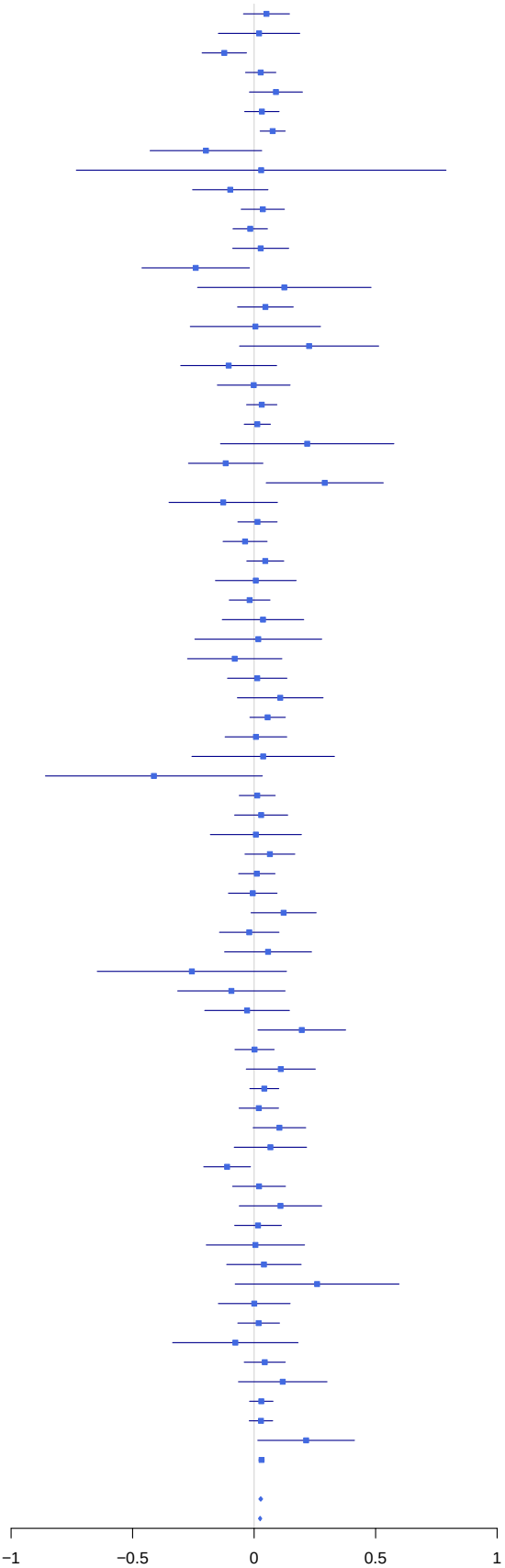
rs61739285, Minor allele/Other allele: T/C (DBP)

Study	Beta(SE)	MAF	N
1958BC	0.029(0.049)	0.0356	5864
ADDITION	0.098(0.076)	0.0399	2307
AGES	0.072(0.066)	0.0222	5526
AIRWAVE	0.053(0.033)	0.0356	13102
ALSPAC	0.011(0.052)	0.0292	6529
ARIC	0.027(0.038)	0.0327	10863
BIOVU	−0.029(0.027)	0.0348	19885
BRIGHTcases	0.014(0.124)	0.0314	1098
BRIGHTcontrols	0.664(0.316)	0.0417	132
CARDIA	0.046(0.09)	0.0299	2175
CCHS	0.039(0.043)	0.0342	8070
CGPS	−0.028(0.037)	0.0313	11783
CHS	−0.042(0.066)	0.0298	4109
CIHDS	0.068(0.108)	0.0314	1434
CROATA−KORCULA	0.075(0.184)	0.0191	814
D2D2007	−0.046(0.065)	0.0486	2580
DIABNORD	−0.1(0.119)	0.0395	912
DPS	−0.33(0.157)	0.0517	416
DRSEXTRA	−0.118(0.109)	0.0615	740
EGCUT	−0.015(0.06)	0.0815	1785
EPIC	0.003(0.032)	0.0315	15674
EPIC−Norfolk	0.034(0.03)	0.0322	17850
ERF	0.394(0.198)	0.0117	1153
FamHS	0.074(0.071)	0.0332	3722
Fenland−CoreExome	−0.099(0.123)	0.0308	1040
Fenland−GWAS	0.258(0.105)	0.0378	1358
Fenland−OMICS	0.08(0.043)	0.0326	8526
FHS	0.037(0.052)	0.0296	7495
FINRISK	−0.041(0.044)	0.0532	5153
FINRISK2007	0.246(0.095)	0.0542	1088
FUSION	−0.044(0.048)	0.0537	4237
GAPP	0.055(0.11)	0.0221	1946
GLACIER	0.189(0.129)	0.0347	922
GoDARTS CAD	−0.022(0.098)	0.0423	1323
GoDARTS	0.051(0.068)	0.0333	3501
GRAPHIC	0.094(0.099)	0.0321	1887
GS	0.023(0.037)	0.0388	9832
HEALTH	0.021(0.063)	0.0373	3674
HELIC−HA	0.198(0.146)	0.026	944
HELIC−HP	−0.613(0.295)	0.0106	565
HRS	−0.026(0.041)	0.0326	9621
HUNT	0.078(0.058)	0.0321	4735
INCIPE	0.062(0.092)	0.0298	1995
INTER99	0.011(0.049)	0.0366	5984
InterAct−CoreExome	0.079(0.039)	0.0311	10915
InterAct−GWAS	−0.023(0.049)	0.0337	6675
INV SC	0.059(0.073)	0.0394	2461
INV UK	0.113(0.069)	0.0344	3242
IPM	0.056(0.126)	0.0251	1342
LBC1921	−0.137(0.202)	0.0335	359
LBC1936	−0.075(0.138)	0.0358	783
LIFELINES	0.057(0.104)	0.0246	1948
LRGP	0.008(0.087)	0.0288	2306
MDC	0.066(0.042)	0.036	8268
MESA	0.23(0.089)	0.0255	2505
METSIM	−0.007(0.034)	0.0554	8411
MORGAM	0.017(0.044)	0.0458	5757
NEO	−0.03(0.059)	0.0235	6115
NFBC66	0.043(0.082)	0.0576	1353
NFBC86full	0.011(0.053)	0.0544	3639
OxBB	0.056(0.059)	0.0325	4440
PIVUSULSAM	0.175(0.081)	0.0398	1998
PPP	0.054(0.048)	0.0488	4766
PROSPER	−0.139(0.108)	0.0341	1275
SDC	0.05(0.185)	0.0311	498
SHIP	0.017(0.043)	0.0401	7160
TwinsUK	−0.018(0.141)	0.0363	689
UKHLS	−0.093(0.044)	0.035	7462
VEJLECASES	−0.021(0.086)	0.0355	2002
WGHS	0.035(0.027)	0.0323	21964
WHI	0.085(0.027)	0.0314	21841
WOSCOPS	0.073(0.108)	0.034	1337
UKBiobank	0.03(0.006)	0.0342	445360
Stage 1	**0.028(0.004)**	**0.0353**	**801220**
Stage 2	**0.023(0.004)**	**0.0342**	**1155020**



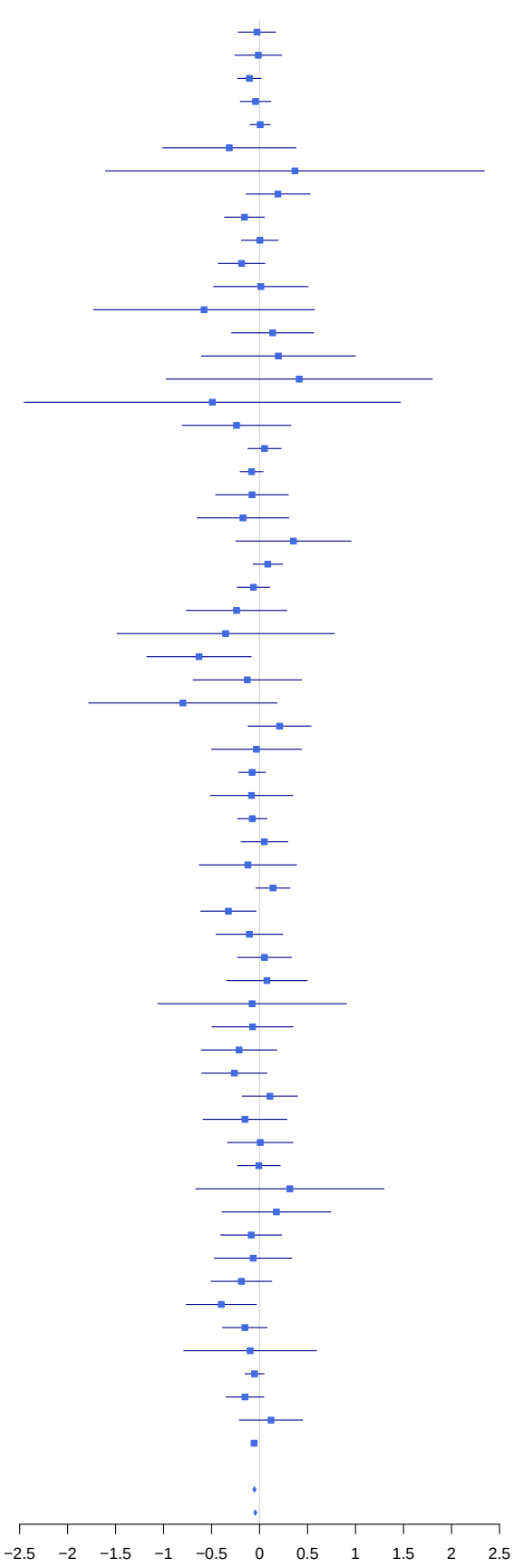
rs61747728, Minor allele/Other allele: T/C (DBP)

Study	Beta(SE)	MAF	N
1958BC	0.051(0.048)	0.0385	5864
ADDITION	0.02(0.085)	0.0295	2307
AGES	−0.123(0.047)	0.0438	5526
AIRWAVE	0.027(0.032)	0.0395	13102
ALSPAC	0.09(0.056)	0.0263	6529
ARIC	0.032(0.036)	0.0371	10863
BIOVU	0.076(0.026)	0.0378	19885
BRIGHTcases	−0.198(0.117)	0.0346	1098
BRIGHTcontrols	0.029(0.388)	0.0265	132
CARDIA	−0.098(0.079)	0.0393	2175
CCHS	0.036(0.045)	0.0314	8070
CGPS	−0.016(0.036)	0.0335	11783
CHS	0.027(0.059)	0.0374	4109
CIHDS	−0.24(0.113)	0.0282	1434
CROATA−KORCULA	0.124(0.182)	0.0203	814
D2D2007	0.046(0.058)	0.0628	2580
DIABNORD	0.005(0.137)	0.0312	912
DPS	0.226(0.146)	0.0613	416
DRSEXTRA	−0.105(0.101)	0.0676	740
EGCUT	−0.002(0.076)	0.0496	1785
EPIC	0.031(0.032)	0.0326	15674
EPIC−Norfolk	0.013(0.027)	0.0384	17850
ERF	0.218(0.182)	0.0147	1153
FamHS	−0.117(0.078)	0.0267	3722
Fenland−CoreExome	0.291(0.123)	0.0341	1040
Fenland−GWAS	−0.127(0.114)	0.0387	1358
Fenland−OMICS	0.014(0.041)	0.0354	8526
FHS	−0.037(0.046)	0.0375	7495
FINRISK	0.046(0.039)	0.0703	5153
FINRISK2007	0.007(0.085)	0.0717	1088
FUSION	−0.018(0.043)	0.0686	4237
GAPP	0.037(0.086)	0.0367	1946
GLACIER	0.017(0.133)	0.0315	922
GoDARTS CAD	−0.08(0.099)	0.0393	1323
GoDARTS	0.013(0.062)	0.0404	3501
GRAPHIC	0.108(0.09)	0.0366	1887
GS	0.056(0.037)	0.0394	9832
HEALTH	0.008(0.065)	0.0335	3674
HELIC−HA	0.037(0.15)	0.0244	944
HELIC−HP	−0.412(0.228)	0.0195	565
HRS	0.013(0.038)	0.038	9621
HUNT	0.029(0.056)	0.0341	4735
INCIPE	0.007(0.096)	0.0286	1995
INTER99	0.065(0.052)	0.0325	5984
InterAct−CoreExome	0.011(0.038)	0.0327	10915
InterAct−GWAS	−0.006(0.051)	0.0347	6675
INV SC	0.121(0.068)	0.0453	2461
INV UK	−0.02(0.062)	0.041	3242
IPM	0.057(0.091)	0.0451	1342
LBC1921	−0.256(0.199)	0.0348	359
LBC1936	−0.093(0.113)	0.0511	783
LIFELINES	−0.029(0.089)	0.0334	1948
LRGP	0.196(0.092)	0.0252	2306
MDC	0.002(0.041)	0.0364	8268
MESA	0.11(0.072)	0.0387	2505
METSIM	0.042(0.03)	0.0713	8411
MORGAM	0.019(0.041)	0.0538	5757
NEO	0.104(0.055)	0.0276	6115
NFBC66	0.067(0.076)	0.0661	1353
NFBC86full	−0.111(0.049)	0.0617	3639
OxBB	0.02(0.056)	0.0389	4440
PIVUSULSAM	0.109(0.087)	0.0355	1998
PPP	0.016(0.049)	0.0468	4766
PROSPER	0.005(0.103)	0.04	1275
RS	0.04(0.078)	0.0299	2875
SDC	0.259(0.172)	0.0341	498
SDR−ANDIS	0.001(0.075)	0.0357	2636
SHIP	0.019(0.044)	0.0381	7160
TwinsUK	−0.077(0.132)	0.0443	689
UKHLS	0.044(0.043)	0.0372	7462
VEJLECASES	0.118(0.093)	0.0302	2002
WGHS	0.03(0.025)	0.04	21964
WHI	0.028(0.025)	0.0393	21841
WOSCOPS	0.214(0.102)	0.0385	1337
UKBiobank	0.031(0.005)	0.0382	445360
Stage 1	**0.027(0.004)**	**0.0396**	**806731**
Stage 2	**0.025(0.003)**	**0.0394**	**1160530**



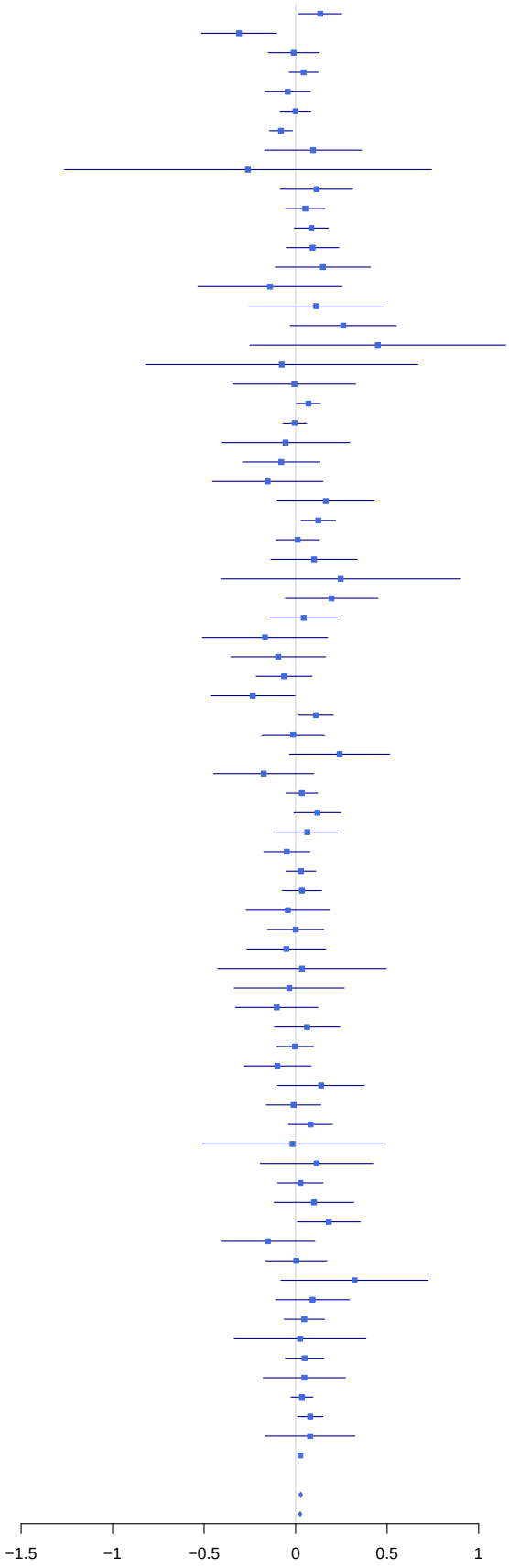
rs61754158, Minor allele/Other allele: T/C (SBP)

Study	Beta(SE)	MAF	N
1958BC	−0.027(0.1)	0.0086	5864
AGES	−0.013(0.124)	0.006	5526
AIRWAVE	−0.106(0.062)	0.01	13102
ARIC	−0.041(0.081)	0.0071	10864
BIOVU	0.006(0.053)	0.0092	19885
BRIGHTcases	−0.315(0.354)	0.0036	1098
BRIGHTcontrols	0.368(1.007)	0.0038	132
CARDIA	0.191(0.17)	0.008	2175
CCHS	−0.157(0.106)	0.0055	8070
CGPS	0.003(0.098)	0.0045	11784
CHS	−0.188(0.124)	0.008	4113
CIHDS	0.013(0.251)	0.0056	1436
CROATA−KORCULA	−0.578(0.588)	0.0018	814
D2D2007	0.136(0.218)	0.0041	2580
DIABNORD	0.196(0.409)	0.0033	912
DPS	0.413(0.708)	0.0024	416
DRSEXTRA	−0.492(1)	7e−04	740
EGCUT	−0.24(0.289)	0.0034	1785
EPIC	0.052(0.088)	0.0041	15676
EPIC−Norfolk	−0.083(0.061)	0.0077	17850
FamHS	−0.079(0.193)	0.0042	3722
Fenland−CoreExome	−0.173(0.244)	0.0082	1040
Fenland−GWAS	0.352(0.307)	0.006	1358
Fenland−OMICS	0.085(0.079)	0.0093	8526
FHS	−0.064(0.087)	0.0106	7495
FINRISK	−0.24(0.267)	0.0014	5152
FINRISK2007	−0.354(0.577)	0.0014	1088
FUSION	−0.631(0.278)	0.0015	4237
GAPP	−0.128(0.289)	0.0031	1947
GLACIER	−0.799(0.501)	0.0022	922
GoDARTS CAD	0.209(0.168)	0.014	1323
GRAPHIC	−0.033(0.239)	0.0056	1887
GS	−0.078(0.071)	0.0103	9832
HELIC−HA	−0.084(0.22)	0.0117	944
HRS	−0.076(0.078)	0.0086	9621
HUNT	0.05(0.124)	0.0068	4735
INCIPE	−0.122(0.259)	0.0038	1995
InterAct−CoreExome	0.14(0.09)	0.0055	10915
InterAct−GWAS	−0.325(0.148)	0.0049	6675
INV SC	−0.106(0.178)	0.0065	2461
INV UK	0.051(0.144)	0.0072	3242
IPM	0.077(0.215)	0.0075	1337
LBC1921	−0.078(0.502)	0.0056	359
LBC1936	−0.073(0.216)	0.014	783
LIFELINES	−0.214(0.201)	0.0064	1948
LRGP	−0.262(0.173)	0.0074	2306
MESA	0.108(0.147)	0.009	2505
METSIM	−0.152(0.223)	0.0012	8411
MORGAM	0.007(0.174)	0.0029	5757
NEO	−0.008(0.114)	0.0064	6117
NFBC66	0.315(0.501)	0.0015	1353
NFBC86full	0.176(0.289)	0.0017	3639
PPP	−0.087(0.163)	0.0038	4766
PROSPER	−0.067(0.206)	0.0094	1275
RS	−0.189(0.161)	0.0068	2875
SDR−ANDIS	−0.399(0.187)	0.0055	2636
SHIP	−0.153(0.118)	0.005	7161
UKHLS	−0.098(0.353)	5e−04	7462
WGHS	−0.052(0.051)	0.0087	21964
WHI	−0.152(0.1)	0.0071	21841
WOSCOPS	0.119(0.169)	0.0127	1337
UKBiobank	−0.057(0.011)	0.0094	445360
Stage 1	**−0.054(0.009)**	**0.0089**	**765131**
Stage 2	**−0.045(0.008)**	**0.0086**	**1119230**



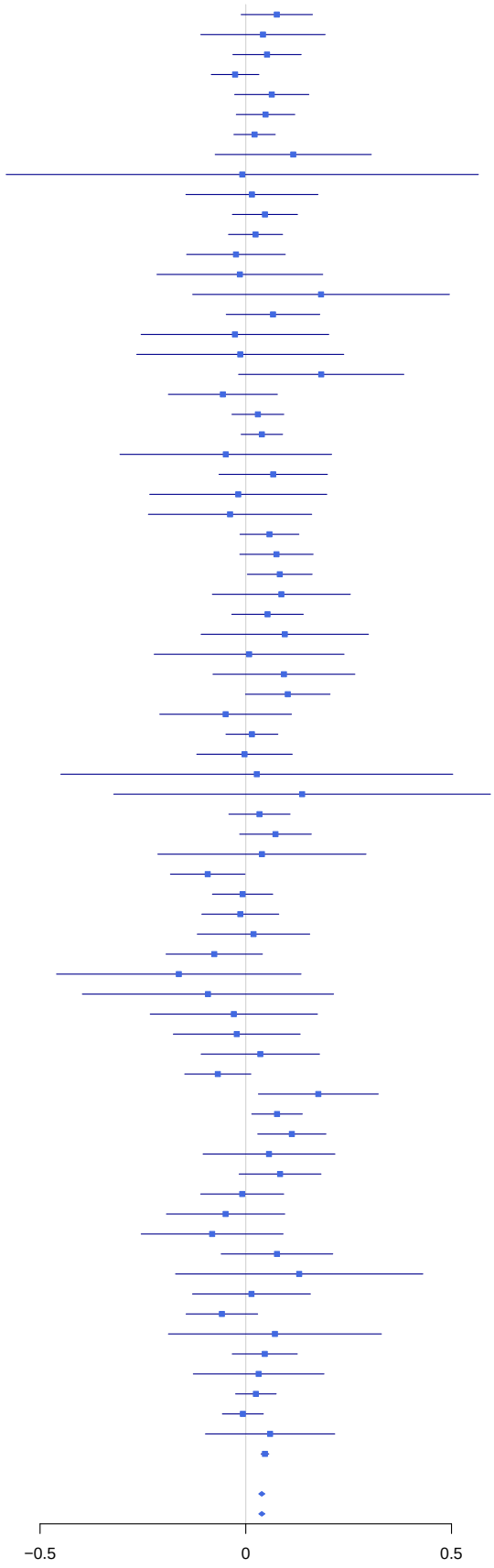
rs61755724, Minor allele/Other allele: A/G (DBP)

Study	Beta(SE)	MAF	N
1958BC	0.134(0.06)	0.0241	5864
ADDITION	−0.309(0.105)	0.0202	2307
AGES	−0.011(0.071)	0.0193	5526
AIRWAVE	0.044(0.04)	0.0239	13102
ALSPAC	−0.043(0.063)	0.0198	6529
ARIC	−0.001(0.042)	0.0264	10863
BIOVU	−0.08(0.032)	0.0249	19885
BRIGHTcases	0.095(0.135)	0.0241	1098
BRIGHTcontrols	−0.26(0.511)	0.0152	132
CARDIA	0.114(0.101)	0.0237	2175
CCHS	0.053(0.055)	0.021	8070
CGPS	0.086(0.048)	0.0191	11783
CHS	0.093(0.073)	0.0229	4109
CIHDS	0.149(0.133)	0.0199	1434
CROATA−KORCULA	−0.14(0.201)	0.0166	814
D2D2007	0.112(0.186)	0.0056	2580
DIABNORD	0.26(0.148)	0.0263	912
DPS	0.45(0.356)	0.0096	416
DRSEXTRA	−0.076(0.379)	0.0047	740
EGCUT	−0.007(0.171)	0.0098	1785
EPIC	0.07(0.034)	0.0286	15674
EPIC−Norfolk	−0.005(0.033)	0.0264	17850
ERF	−0.055(0.179)	0.0147	1153
FamHS	−0.078(0.108)	0.013	3722
Fenland−CoreExome	−0.153(0.154)	0.0212	1040
Fenland−GWAS	0.165(0.134)	0.0246	1358
Fenland−OMICS	0.124(0.048)	0.026	8526
FHS	0.011(0.06)	0.0217	7495
FINRISK	0.101(0.12)	0.0068	5153
FINRISK2007	0.246(0.334)	0.0041	1088
FUSION	0.196(0.129)	0.007	4237
GAPP	0.044(0.095)	0.0303	1946
GLACIER	−0.167(0.175)	0.0184	922
GoDARTS CAD	−0.095(0.132)	0.0227	1323
GoDARTS	−0.063(0.078)	0.0244	3501
GRAPHIC	−0.234(0.117)	0.0217	1887
GS	0.111(0.048)	0.0227	9832
HEALTH	−0.013(0.087)	0.0182	3674
HELIC−HA	0.241(0.14)	0.0291	944
HELIC−HP	−0.174(0.14)	0.0513	565
HRS	0.034(0.044)	0.0269	9621
HUNT	0.119(0.065)	0.0249	4735
INCIPE	0.064(0.086)	0.0356	1995
INTER99	−0.048(0.064)	0.0207	5984
InterAct−CoreExome	0.029(0.042)	0.0265	10915
InterAct−GWAS	0.035(0.055)	0.0287	6675
INV SC	−0.042(0.116)	0.0156	2461
INV UK	0.001(0.079)	0.0248	3242
IPM	−0.051(0.11)	0.0313	1342
LBC1921	0.035(0.235)	0.0265	359
LBC1936	−0.035(0.154)	0.0255	783
LIFELINES	−0.103(0.115)	0.0203	1948
LRGP	0.063(0.091)	0.026	2306
MDC	−0.003(0.052)	0.0228	8268
MESA	−0.099(0.094)	0.0234	2505
METSIM	0.14(0.121)	0.0041	8411
MORGAM	−0.011(0.076)	0.0155	5757
NEO	0.081(0.061)	0.0214	6115
NFBC66	−0.017(0.251)	0.0059	1353
NFBC86full	0.115(0.157)	0.0056	3639
OxBB	0.026(0.064)	0.0286	4440
PIVUSULSAM	0.1(0.111)	0.0205	1998
PPP	0.181(0.088)	0.0136	4766
PROSPER	−0.151(0.131)	0.0231	1275
RS	0.004(0.086)	0.0249	2875
SDC	0.322(0.205)	0.0251	498
SDR−ANDIS	0.093(0.103)	0.0186	2636
SHIP	0.048(0.056)	0.0224	7160
TwinsUK	0.024(0.184)	0.0225	689
UKHLS	0.049(0.054)	0.0238	7462
VEJLECASES	0.048(0.115)	0.0197	2002
WGHS	0.035(0.031)	0.0247	21964
WHI	0.08(0.035)	0.0251	21841
WOSCOPS	0.079(0.125)	0.0236	1337
UKBiobank	0.026(0.007)	0.0239	445360
Stage 1	**0.028(0.005)**	**0.0239**	**806731**
Stage 2	**0.025(0.004)**	**0.024**	**1160530**



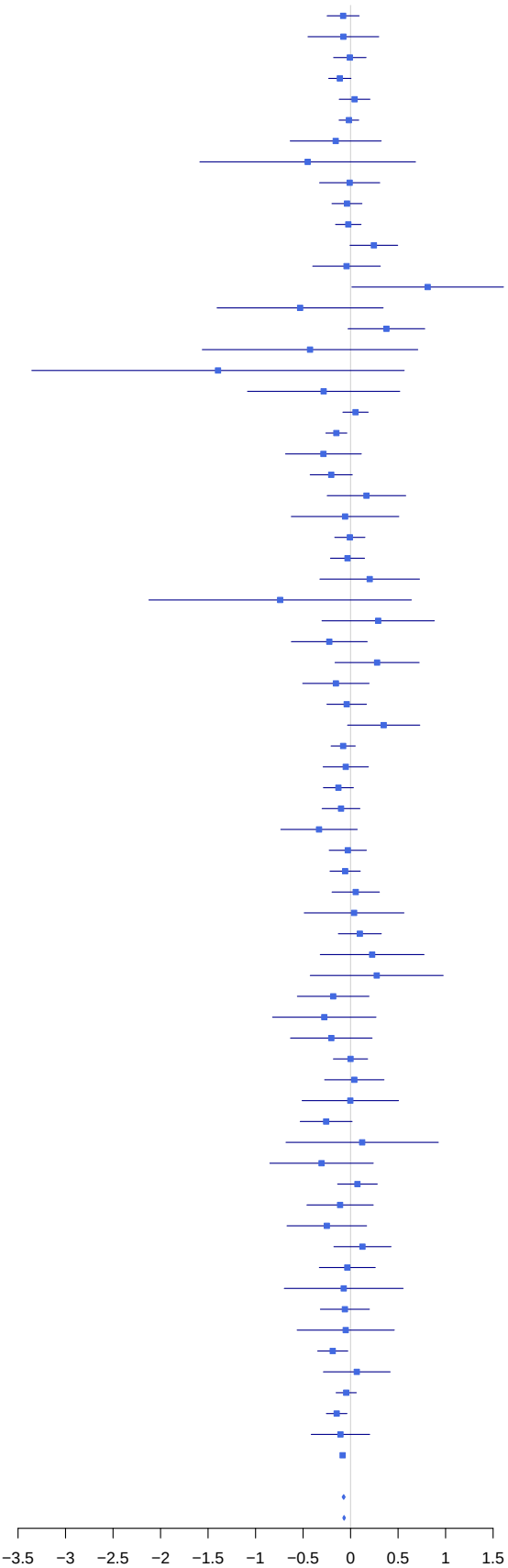
rs62051555, Minor allele/Other allele: G/C (PP)

Study	Beta(SE)	MAF	N
1958BC	0.075(0.044)	0.0468	5861
ADDITION	0.042(0.077)	0.0382	2306
AGES	0.052(0.042)	0.0605	5526
AIRWAVE	−0.026(0.029)	0.0501	13102
ALSPAC	0.063(0.046)	0.0389	6529
ARIC	0.048(0.036)	0.0382	10863
BIOVU	0.021(0.026)	0.0408	19885
BRIGHTcases	0.115(0.097)	0.051	1098
BRIGHTcontrols	−0.009(0.293)	0.0492	132
CARDIA	0.015(0.082)	0.0354	2175
CCHS	0.047(0.04)	0.0415	8070
CGPS	0.024(0.034)	0.0415	11783
CHS	−0.024(0.061)	0.0346	4109
CIHDS	−0.014(0.103)	0.0356	1434
CROATA	0.183(0.159)	0.027	814
D2D2007	0.066(0.058)	0.0641	2580
DIABNORD	−0.026(0.116)	0.0378	912
DPS	−0.013(0.128)	0.0781	416
DRSEXTRA	0.183(0.102)	0.0669	740
EGCUT	−0.056(0.068)	0.0661	1785
EPIC	0.029(0.032)	0.0338	15673
EPIC−Norfolk	0.039(0.026)	0.0441	17850
ERF	−0.049(0.131)	0.026	1152
FamHS	0.067(0.067)	0.0361	3722
Fenland−CoreExome	−0.018(0.11)	0.0438	1040
Fenland−GWAS	−0.038(0.101)	0.0398	1358
Fenland−OMICS	0.058(0.037)	0.0456	8526
FHS	0.075(0.045)	0.0377	7495
FINRISK	0.083(0.04)	0.0653	5152
FINRISK2007	0.086(0.086)	0.0676	1088
FUSION	0.053(0.044)	0.0642	4237
GAPP	0.095(0.104)	0.0249	1946
GLACIER	0.008(0.118)	0.0401	922
GoDARTS CAD	0.093(0.088)	0.0552	1323
GoDARTS	0.102(0.052)	0.0563	3501
GRAPHIC	−0.049(0.082)	0.048	1887
GS	0.015(0.032)	0.0577	9832
HEALTH	−0.003(0.059)	0.0414	3674
HELIC−HA	0.027(0.243)	0.0095	944
HELIC−HP	0.137(0.234)	0.0168	565
HRS	0.033(0.038)	0.0379	9621
HUNT	0.072(0.044)	0.0546	4735
INCIPE	0.039(0.129)	0.0155	1995
INTER99	−0.093(0.046)	0.0417	5983
InterAct−CoreExome	−0.008(0.037)	0.0359	10915
InterAct−GWAS	−0.013(0.048)	0.0351	6675
INV SC	0.019(0.07)	0.0453	2461
INV UK	−0.077(0.06)	0.047	3242
IPM	−0.163(0.152)	0.0168	1337
LBC1921	−0.092(0.156)	0.0585	359
LBC1936	−0.029(0.104)	0.067	783
LIFELINES	−0.022(0.079)	0.0444	1948
LRGP	0.035(0.073)	0.0416	2306
MDC	−0.068(0.041)	0.0389	8268
MESA	0.176(0.074)	0.0377	2505
METSIM	0.076(0.031)	0.0756	8411
MORGAM	0.112(0.042)	0.0545	5757
NFBC66	0.056(0.082)	0.0584	1353
NFBC86full	0.083(0.051)	0.0568	3639
OxBB	−0.009(0.051)	0.0444	4440
PIVUSULSAM	−0.049(0.073)	0.049	1998
PROSPER	−0.082(0.088)	0.0553	1275
RS	0.076(0.069)	0.0374	2875
SDC	0.13(0.153)	0.0423	497
SDR−ANDIS	0.014(0.073)	0.037	2634
SHIP	−0.058(0.044)	0.0379	7159
TwinsUK	0.071(0.132)	0.0457	689
UKHLS	0.046(0.04)	0.0443	7462
VEJLECASES	0.031(0.081)	0.0391	1996
WGHS	0.025(0.025)	0.0386	21964
WHI	−0.007(0.025)	0.0366	21841
WOSCOPS	0.059(0.08)	0.0572	1337
UKBiobank	0.047(0.005)	0.0487	445360
Stage 1	**0.039(0.004)**	**0.0476**	**795827**
Stage 2	**0.039(0.004)**	**0.0476**	**797332**



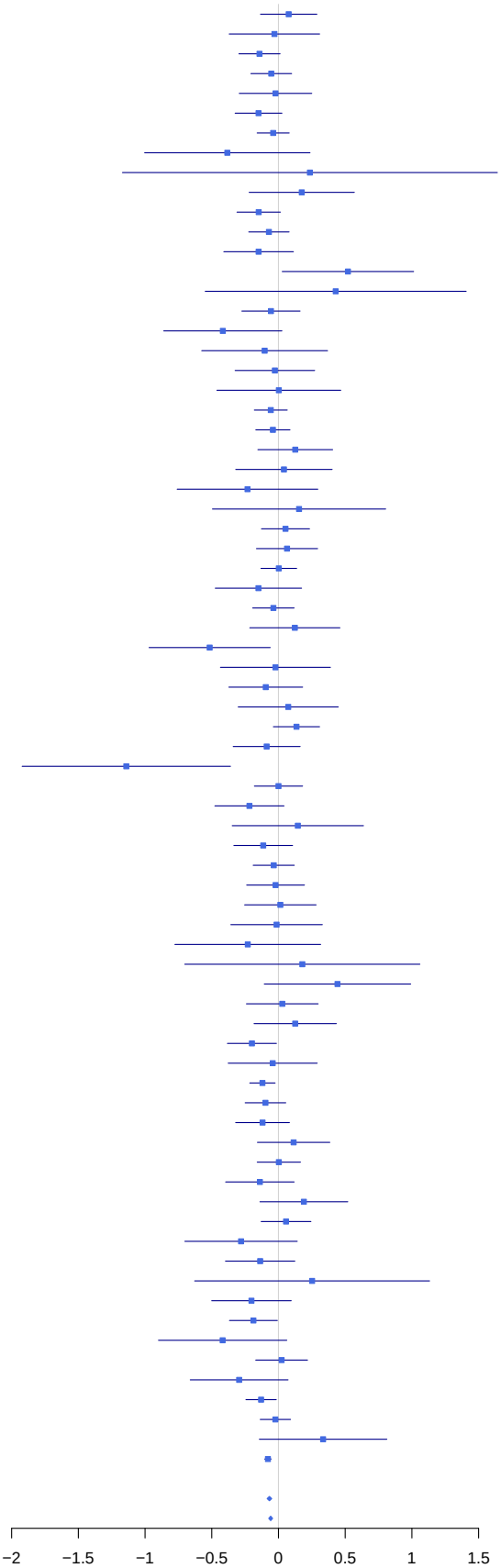
rs72681869, Minor allele/Other allele: C/G (SBP)

Study	Beta(SE)	MAF	N
1958BC	−0.078(0.086)	0.0119	5864
ADDITION	−0.076(0.19)	0.0061	2307
AGES	−0.008(0.087)	0.0128	5526
AIRWAVE	−0.113(0.06)	0.0109	13102
ARIC	0.042(0.082)	0.0068	10864
BIOVU	−0.018(0.053)	0.0092	19885
BRIGHTcases	−0.157(0.244)	0.0077	1098
BRIGHTcontrols	−0.452(0.579)	0.0114	132
CARDIA	−0.01(0.161)	0.009	2175
CCHS	−0.038(0.081)	0.0097	8070
CGPS	−0.024(0.068)	0.0093	11784
CHS	0.245(0.128)	0.0073	4113
CIHDS	−0.043(0.181)	0.0108	1436
CROATA−KORCULA	0.811(0.407)	0.0037	814
D2D2007	−0.531(0.446)	0.001	2580
DIABNORD	0.377(0.206)	0.011	912
DPS	−0.427(0.579)	0.0036	416
DRSEXTRA	−1.395(1)	7e−04	740
EGCUT	−0.283(0.409)	0.0017	1785
EPIC	0.052(0.068)	0.007	15676
EPIC−Norfolk	−0.15(0.056)	0.0096	17850
ERF	−0.286(0.203)	0.0121	1153
FamHS	−0.204(0.113)	0.0128	3722
Fenland−CoreExome	0.167(0.211)	0.0111	1040
Fenland−GWAS	−0.058(0.289)	0.0066	1358
Fenland−OMICS	−0.008(0.081)	0.0096	8526
FHS	−0.032(0.091)	0.0089	7495
FINRISK	0.201(0.267)	0.0014	5152
FINRISK2007	−0.741(0.705)	9e−04	1088
FUSION	0.29(0.302)	0.0013	4237
GAPP	−0.224(0.204)	0.0062	1947
GLACIER	0.279(0.226)	0.0108	922
GoDARTS CAD	−0.155(0.178)	0.0121	1323
GoDARTS	−0.041(0.106)	0.013	3501
GRAPHIC	0.349(0.194)	0.0079	1887
GS	−0.078(0.065)	0.0125	9832
HEALTH	−0.051(0.122)	0.0094	3674
HRS	−0.128(0.08)	0.0082	9621
HUNT	−0.101(0.101)	0.01	4735
INCIPE	−0.332(0.205)	0.006	1995
INTER99	−0.029(0.1)	0.0085	5986
InterAct−CoreExome	−0.057(0.081)	0.0071	10915
InterAct−GWAS	0.054(0.127)	0.0066	6675
INV SC	0.037(0.268)	0.0028	2461
INV UK	0.097(0.115)	0.0119	3242
IPM	0.227(0.279)	0.0049	1337
LBC1921	0.275(0.357)	0.0111	359
LBC1936	−0.183(0.192)	0.0179	783
LIFELINES	−0.277(0.278)	0.0033	1948
LRGP	−0.203(0.219)	0.0046	2306
MDC	−0.001(0.092)	0.0073	8268
MESA	0.039(0.159)	0.008	2505
METSIM	−0.003(0.259)	9e−04	8411
MORGAM	−0.257(0.139)	0.0043	5757
NFBC66	0.122(0.409)	0.0022	1353
NFBC86full	−0.305(0.278)	0.0018	3639
OxBB	0.072(0.106)	0.0099	4440
PIVUSULSAM	−0.11(0.178)	0.008	1998
PPP	−0.25(0.214)	0.0023	4766
PROSPER	0.125(0.153)	0.0173	1275
RS	−0.035(0.15)	0.0075	2875
SDC	−0.072(0.319)	0.01	498
SHIP	−0.06(0.132)	0.0039	7161
TwinsUK	−0.051(0.261)	0.0109	689
UKHLS	−0.188(0.081)	0.0102	7462
VEJLECASES	0.065(0.179)	0.008	1996
WGHS	−0.046(0.054)	0.0078	21964
WHI	−0.146(0.055)	0.0075	21841
WOSCOPS	−0.107(0.157)	0.0157	1337
UKBiobank	−0.084(0.01)	0.0109	445360
Stage 1	**−0.073(0.008)**	**0.0103**	**789944**
Stage 2	**−0.068(0.007)**	**0.01**	**1144040**



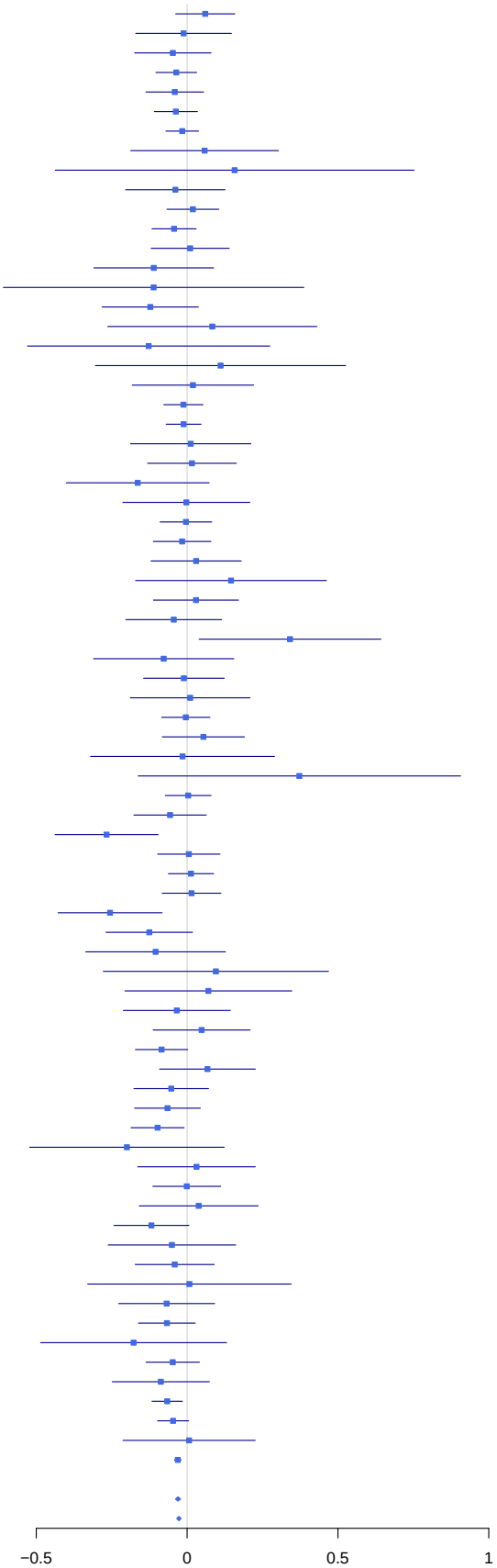
rs73181210, Minor allele/Other allele: C/T (DBP)

Study	Beta(SE)	MAF	N
1958BC	0.077(0.108)	0.0074	5864
ADDITION	−0.03(0.173)	0.0074	2307
AGES	−0.142(0.079)	0.015	5526
AIRWAVE	−0.054(0.078)	0.0063	13102
ALSPAC	−0.022(0.139)	0.0041	6529
ARIC	−0.149(0.09)	0.0059	10863
BIOVU	−0.04(0.061)	0.0067	19885
BRIGHTcases	−0.383(0.316)	0.0046	1098
BRIGHTcontrols	0.236(0.717)	0.0076	132
CARDIA	0.174(0.201)	0.0057	2175
CCHS	−0.148(0.083)	0.009	8070
CGPS	−0.072(0.077)	0.0073	11783
CHS	−0.149(0.133)	0.0069	4109
CIHDS	0.521(0.251)	0.0056	1434
CROATA−KORCULA	0.429(0.499)	0.0025	814
D2D2007	−0.056(0.111)	0.0159	2580
DIABNORD	−0.417(0.226)	0.011	912
DPS	−0.104(0.241)	0.0216	416
DRSEXTRA	−0.027(0.152)	0.0311	740
EGCUT	0.003(0.237)	0.005	1785
EPIC	−0.058(0.063)	0.0082	15674
EPIC−Norfolk	−0.042(0.065)	0.0066	17850
ERF	0.126(0.143)	0.0243	1153
FamHS	0.041(0.184)	0.0044	3722
Fenland−CoreExome	−0.232(0.269)	0.0067	1040
Fenland−GWAS	0.154(0.331)	0.0051	1358
Fenland−OMICS	0.053(0.092)	0.0069	8526
FHS	0.064(0.117)	0.0056	7495
FINRISK	0.002(0.068)	0.0214	5153
FINRISK2007	−0.15(0.165)	0.0175	1088
FUSION	−0.038(0.079)	0.0189	4237
GAPP	0.123(0.172)	0.009	1946
GLACIER	−0.516(0.232)	0.0103	922
GoDARTS CAD	−0.023(0.21)	0.0087	1323
GoDARTS	−0.095(0.141)	0.0073	3501
GRAPHIC	0.073(0.191)	0.0079	1887
GS	0.135(0.088)	0.0067	9832
HEALTH	−0.089(0.128)	0.0082	3674
HELIC−HP	−1.141(0.398)	0.0062	565
HRS	0(0.092)	0.0061	9621
HUNT	−0.218(0.132)	0.0061	4735
INCIPE	0.145(0.251)	0.004	1995
INTER99	−0.114(0.112)	0.0067	5984
InterAct−CoreExome	−0.035(0.079)	0.0075	10915
InterAct−GWAS	−0.022(0.11)	0.007	6675
INV SC	0.014(0.137)	0.0112	2461
INV UK	−0.014(0.175)	0.0051	3242
IPM	−0.23(0.279)	0.0049	1342
LBC1921	0.179(0.45)	0.007	359
LBC1936	0.442(0.28)	0.0083	783
LIFELINES	0.029(0.137)	0.0141	1948
LRGP	0.125(0.157)	0.0085	2306
MDC	−0.199(0.094)	0.007	8268
MESA	−0.043(0.17)	0.007	2505
METSIM	−0.12(0.048)	0.0275	8411
MORGAM	−0.098(0.078)	0.015	5757
NEO	−0.119(0.103)	0.0079	6115
NFBC66	0.114(0.138)	0.0185	1353
NFBC86full	0.003(0.083)	0.0201	3639
OxBB	−0.139(0.131)	0.0064	4440
PIVUSULSAM	0.19(0.168)	0.009	1998
PPP	0.057(0.095)	0.0115	4766
PROSPER	−0.28(0.215)	0.0086	1275
RS	−0.137(0.133)	0.0101	2875
SDC	0.252(0.449)	0.005	498
SDR−ANDIS	−0.203(0.152)	0.0083	2636
SHIP	−0.188(0.092)	0.0084	7160
TwinsUK	−0.418(0.245)	0.0123	689
UKHLS	0.023(0.099)	0.0069	7462
VEJLECASES	−0.295(0.187)	0.0072	2002
WGHS	−0.13(0.058)	0.0067	21964
WHI	−0.023(0.058)	0.0069	21841
WOSCOPS	0.334(0.244)	0.0064	1337
UKBiobank	−0.079(0.012)	0.0072	445360
Stage 1	**−0.068(0.009)**	**0.0089**	**805787**
Stage 2	**−0.058(0.008)**	**0.009**	**1159580**



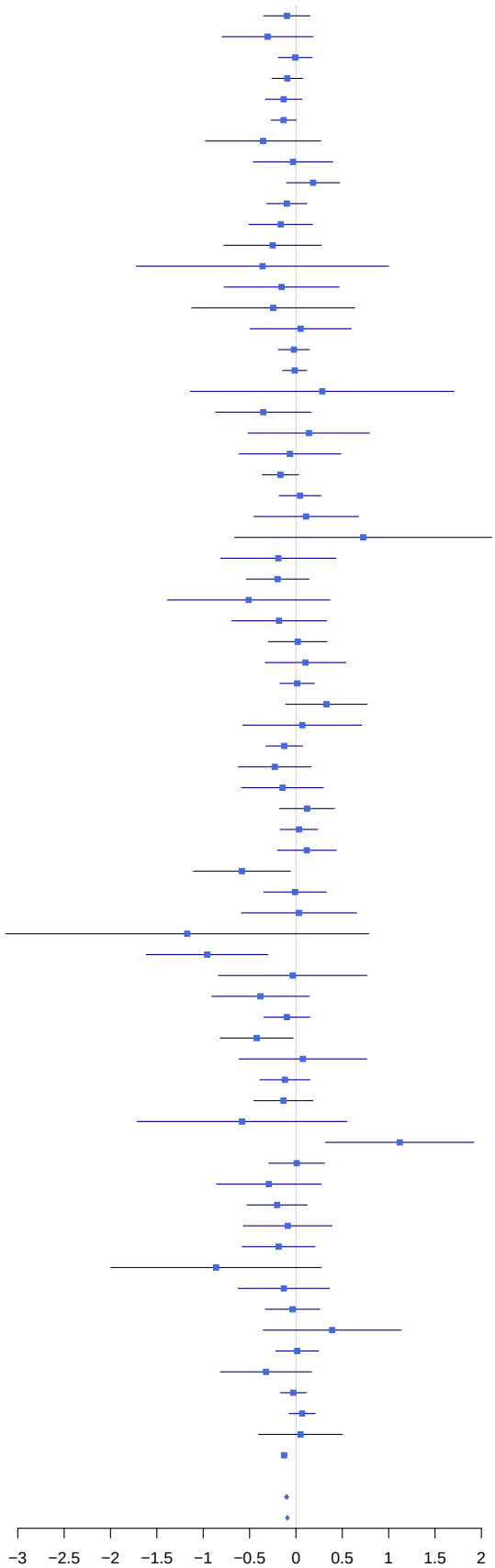
rs76767219, Minor allele/Other allele: A/C (SBP)

Study	Beta(SE)	MAF	N
1958BC	0.06(0.05)	0.0344	5864
ADDITION	−0.012(0.081)	0.0332	2307
AGES	−0.047(0.065)	0.0221	5526
AIRWAVE	−0.036(0.034)	0.0325	13102
ALSPAC	−0.041(0.049)	0.0342	6529
ARIC	−0.037(0.037)	0.0359	10864
BIOVU	−0.016(0.028)	0.0343	19885
BRIGHTcases	0.058(0.125)	0.0301	1098
BRIGHTcontrols	0.157(0.303)	0.0455	132
CARDIA	−0.039(0.084)	0.0349	2175
CCHS	0.019(0.044)	0.0327	8070
CGPS	−0.043(0.037)	0.0313	11784
CHS	0.01(0.066)	0.0288	4113
CIHDS	−0.111(0.101)	0.0341	1436
CROATA−KORCULA	−0.111(0.254)	0.0098	814
D2D2007	−0.122(0.081)	0.0298	2580
DIABNORD	0.084(0.177)	0.017	912
DPS	−0.127(0.205)	0.0276	416
DRSEXTRA	0.111(0.212)	0.0155	740
EGCUT	0.019(0.103)	0.0275	1785
EPIC	−0.012(0.033)	0.0296	15676
EPIC−Norfolk	−0.012(0.03)	0.0334	17850
ERF	0.012(0.102)	0.0486	1153
FamHS	0.016(0.075)	0.0294	3722
Fenland−CoreExome	−0.164(0.121)	0.0332	1040
Fenland−GWAS	−0.002(0.107)	0.0359	1358
Fenland−OMICS	−0.004(0.044)	0.0324	8526
FHS	−0.017(0.049)	0.0338	7495
FINRISK	0.03(0.076)	0.0168	5152
FINRISK2007	0.146(0.161)	0.0184	1088
FUSION	0.029(0.072)	0.0238	4237
GAPP	−0.044(0.081)	0.0421	1947
GLACIER	0.341(0.154)	0.0217	922
GoDARTS CAD	−0.078(0.119)	0.028	1323
GoDARTS	−0.011(0.068)	0.0318	3501
GRAPHIC	0.01(0.101)	0.0294	1887
GS	−0.004(0.041)	0.0321	9832
HEALTH	0.054(0.07)	0.029	3674
HELIC−HA	−0.015(0.156)	0.0228	944
HELIC−HP	0.372(0.273)	0.0124	565
HRS	0.004(0.039)	0.0363	9621
HUNT	−0.056(0.061)	0.0293	4735
INCIPE	−0.267(0.087)	0.0326	1995
INTER99	0.006(0.053)	0.0319	5986
InterAct−CoreExome	0.013(0.038)	0.0331	10915
InterAct−GWAS	0.015(0.05)	0.0333	6675
INV SC	−0.255(0.088)	0.0264	2461
INV UK	−0.125(0.073)	0.0299	3242
IPM	−0.104(0.118)	0.0284	1337
LBC1921	0.095(0.19)	0.0418	359
LBC1936	0.071(0.141)	0.03	783
LIFELINES	−0.034(0.09)	0.0323	1948
LRGP	0.048(0.082)	0.0317	2306
MDC	−0.085(0.044)	0.0318	8268
MESA	0.068(0.081)	0.0321	2505
METSIM	−0.053(0.063)	0.0156	8411
MORGAM	−0.065(0.056)	0.0288	5757
NEO	−0.098(0.045)	0.042	6117
NFBC66	−0.2(0.164)	0.014	1353
NFBC86full	0.031(0.099)	0.014	3639
OxBB	−0.001(0.057)	0.0358	4440
PIVUSULSAM	0.038(0.101)	0.0248	1998
PPP	−0.118(0.063)	0.0271	4766
PROSPER	−0.05(0.108)	0.0345	1275
RS	−0.041(0.067)	0.0414	2875
SDC	0.008(0.172)	0.0341	498
SDR−ANDIS	−0.068(0.081)	0.0298	2636
SHIP	−0.067(0.048)	0.0312	7161
TwinsUK	−0.177(0.157)	0.0312	689
UKHLS	−0.047(0.045)	0.0345	7462
VEJLECASES	−0.087(0.082)	0.0376	1996
WGHS	−0.066(0.026)	0.0355	21964
WHI	−0.046(0.026)	0.0338	21841
WOSCOPS	0.007(0.112)	0.0318	1337
UKBiobank	−0.031(0.006)	0.0345	445360
Stage 1	**−0.03(0.004)**	**0.0337**	**806735**
Stage 2	**−0.027(0.004)**	**0.0332**	**1160830**



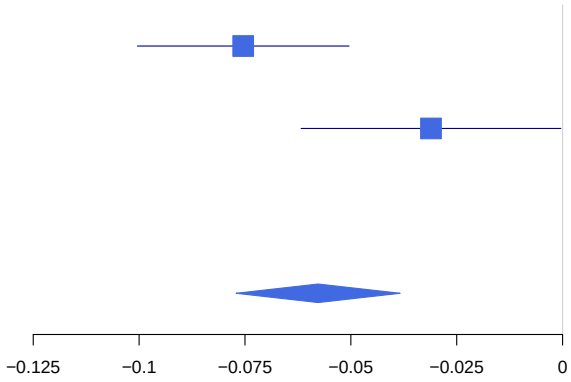
rs77357563, Minor allele/Other allele: A/C (PP)

Study	Beta(SE)	MAF	N
1958BC	−0.097(0.127)	0.0054	5861
ADDITION	−0.306(0.251)	0.0035	2306
AGES	−0.007(0.093)	0.0109	5526
AIRWAVE	−0.093(0.085)	0.0053	13102
ARIC	−0.132(0.101)	0.0046	10863
BIOVU	−0.133(0.069)	0.0054	19885
BRIGHTcases	−0.354(0.317)	0.0046	1098
CARDIA	−0.032(0.219)	0.0048	2175
CCHS	0.185(0.146)	0.0029	8070
CGPS	−0.099(0.11)	0.0034	11783
CHS	−0.164(0.174)	0.004	4109
CIHDS	−0.251(0.268)	0.0049	1434
CROATA	−0.36(0.694)	0.0012	814
D2D2007	−0.155(0.317)	0.0019	2580
DIABNORD	−0.245(0.448)	0.0027	912
EGCUT	0.05(0.278)	0.0036	1785
EPIC	−0.022(0.086)	0.0043	15673
EPIC−Norfolk	−0.013(0.066)	0.0064	17850
ERF	0.284(0.726)	9e−04	1152
FamHS	−0.352(0.263)	0.0023	3722
Fenland−CoreExome	0.14(0.334)	0.0043	1040
Fenland−GWAS	−0.066(0.28)	0.0074	1358
Fenland−OMICS	−0.167(0.1)	0.0059	8526
FHS	0.044(0.115)	0.006	7495
FINRISK	0.109(0.289)	0.0012	5152
FINRISK2007	0.725(0.707)	9e−04	1088
FUSION	−0.19(0.317)	0.0012	4237
GAPP	−0.198(0.173)	0.0087	1946
GLACIER	−0.51(0.448)	0.0027	922
GoDARTS CAD	−0.182(0.261)	0.0057	1323
GoDARTS	0.019(0.161)	0.0056	3501
GRAPHIC	0.103(0.222)	0.0058	1887
GS	0.013(0.095)	0.0057	9832
HEALTH	0.329(0.224)	0.0027	3674
HELIC−HA	0.068(0.328)	0.0053	944
HRS	−0.126(0.1)	0.005	9621
HUNT	−0.228(0.201)	0.0026	4735
INCIPE	−0.145(0.225)	0.005	1995
INTER99	0.12(0.151)	0.0037	5983
InterAct−CoreExome	0.033(0.103)	0.0041	10915
InterAct−GWAS	0.117(0.162)	0.0045	6675
INV SC	−0.583(0.267)	0.0028	2461
INV UK	−0.009(0.172)	0.0052	3242
IPM	0.033(0.317)	0.0037	1337
LBC1921	−1.172(1)	0.0014	359
LBC1936	−0.958(0.335)	0.0057	783
LIFELINES	−0.035(0.409)	0.0015	1948
LRGP	−0.383(0.268)	0.003	2306
MDC	−0.098(0.126)	0.0037	8268
MESA	−0.424(0.201)	0.005	2505
METSIM	0.074(0.352)	5e−04	8411
MORGAM	−0.119(0.138)	0.0046	5757
NEO	−0.135(0.163)	0.0031	6115
NFBC66	−0.582(0.578)	0.0011	1353
NFBC86full	1.119(0.409)	8e−04	3639
OxBB	0.008(0.153)	0.0048	4440
PIVUSULSAM	−0.292(0.288)	0.003	1998
PPP	−0.203(0.165)	0.0039	4766
PROSPER	−0.089(0.244)	0.0067	1275
RS	−0.187(0.201)	0.0043	2875
SDC	−0.862(0.578)	0.003	497
SDR−ANDIS	−0.131(0.251)	0.003	2634
SHIP	−0.037(0.149)	0.0031	7159
TwinsUK	0.391(0.38)	0.0051	689
UKHLS	0.013(0.118)	0.0049	7462
VEJLECASES	−0.322(0.251)	0.004	1996
WGHS	−0.028(0.072)	0.0045	21964
WHI	0.067(0.072)	0.0044	21841
WOSCOPS	0.049(0.231)	0.0071	1337
UKBiobank	−0.128(0.015)	0.005	445360
Stage 1	**−0.1(0.011)**	**0.005**	**798326**
Stage 2	**−0.093(0.01)**	**0.0053**	**1152080**



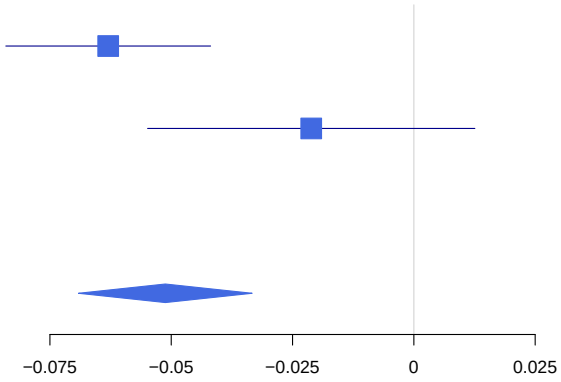
rs114026228, Effect allele/Other allele: C/T (PP)

Study	Beta(SE)	MAF	N
UKBiobank	−0.075(0.013)	0.0082	445360
MVP	−0.031(0.016)	0.018	224768
UKBiobank+MVP	**−0.058(0.01)**	**0.0121**	**670128**



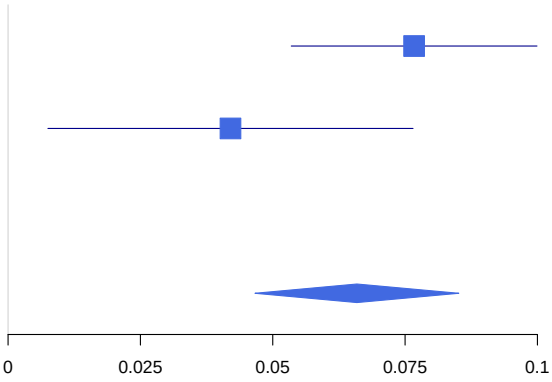
rs114580352, Effect allele/Other allele: A/G (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	−0.063(0.011)	0.0093	445360
MVP	−0.021(0.017)	0.0094	220500
UKBiobank+MVP	**−0.051(0.009)**	**0.0094**	**665860**



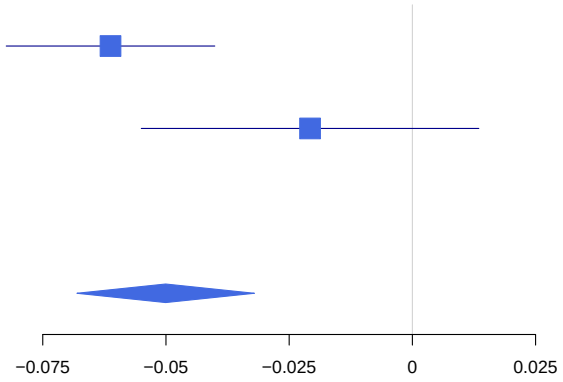
rs117627418, Effect allele/Other allele: T/C (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	0.077(0.012)	0.0086	445360
MVP	0.042(0.018)	0.0082	220501
UKBiobank+MVP	**0.066(0.01)**	**0.0085**	**665861**



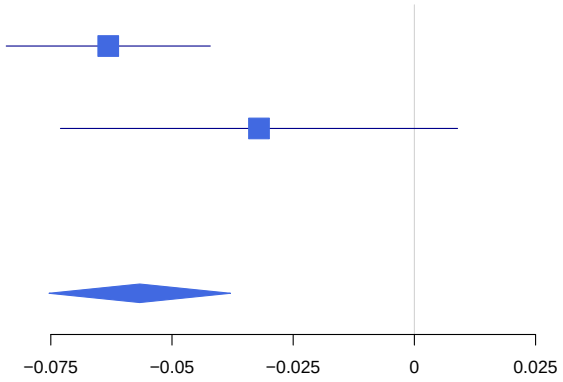
rs11907239, Effect allele/Other allele: A/G (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	−0.061(0.011)	0.0092	445360
MVP	−0.021(0.017)	0.0088	225112
UKBiobank+MVP	**−0.05(0.009)**	**0.0091**	**670472**



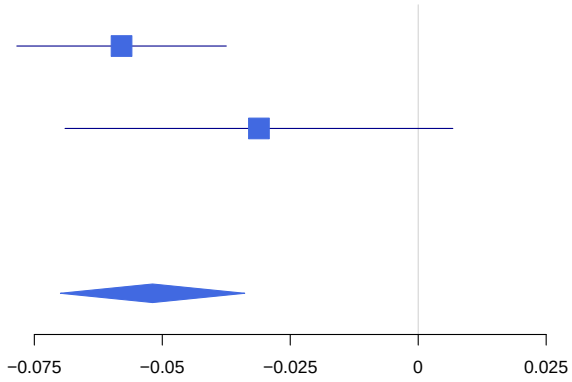
rs12128471, Effect allele/Other allele: A/G (PP)

Study	Beta(SE)	MAF	N
UKBiobank	−0.063(0.011)	0.0095	445360
MVP	−0.032(0.021)	0.0077	224770
UKBiobank+MVP	**−0.057(0.01)**	**0.0091**	**670130**



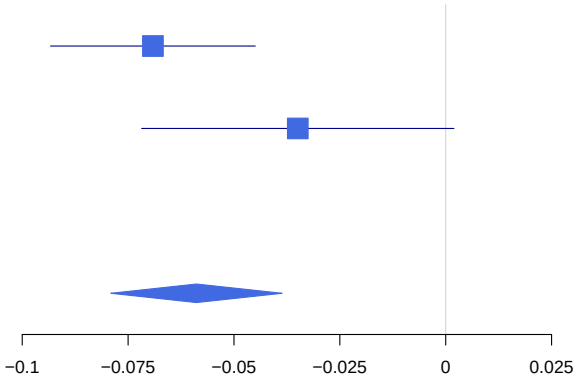
rs12135454, Effect allele/Other allele: T/C (PP)

Study	Beta(SE)	MAF	N
UKBiobank	−0.058(0.01)	0.01	445360
MVP	−0.031(0.019)	0.0077	220163
UKBiobank+MVP	**−0.052(0.009)**	**0.0095**	**665523**



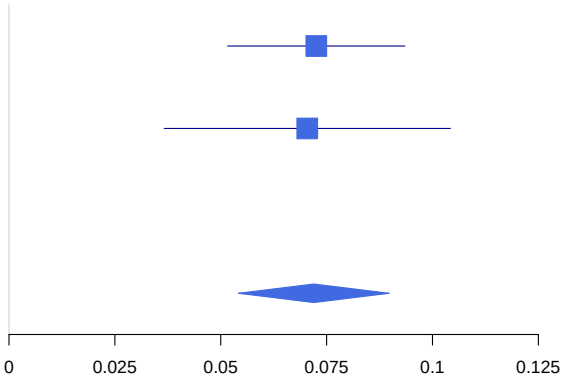
rs138656258, Effect allele/Other allele: G/T (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	−0.069(0.012)	0.0074	445360
MVP	−0.035(0.019)	0.0072	220501
UKBiobank+MVP	**−0.059(0.01)**	**0.0073**	**665861**



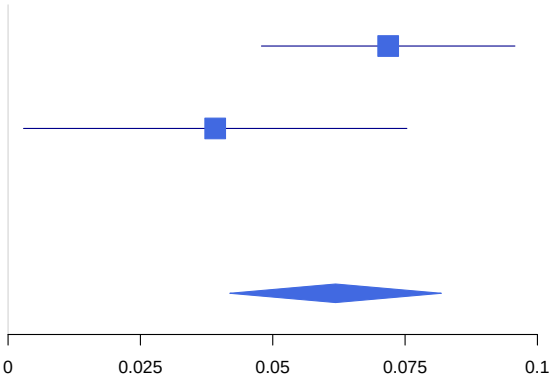
rs142760284, Effect allele/Other allele: A/C (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	0.073(0.011)	0.0094	445360
MVP	0.07(0.017)	0.0078	225112
UKBiobank+MVP	**0.072(0.009)**	**0.009**	**670472**



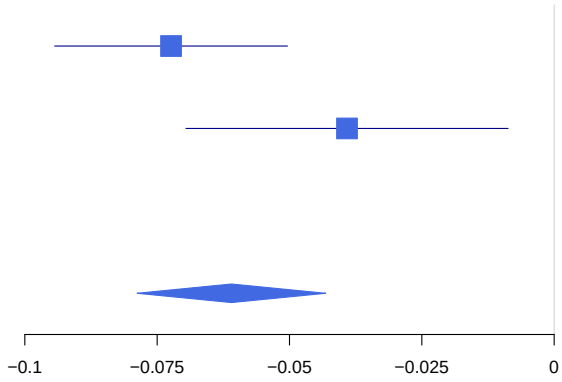
rs143554274, Effect allele/Other allele: T/C (PP)

Study	Beta(SE)	MAF	N
UKBiobank	0.072(0.012)	0.0081	445360
MVP	0.039(0.018)	0.012	224768
UKBiobank+MVP	**0.062(0.01)**	**0.0093**	**670128**



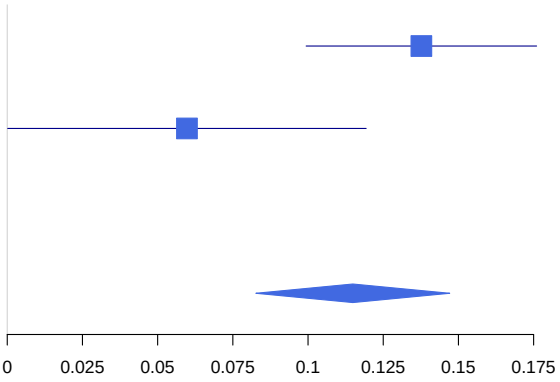
rs145441283, Effect allele/Other allele: G/A (PP)

Study	Beta(SE)	MAF	N
UKBiobank	−0.072(0.011)	0.0098	445360
MVP	−0.039(0.016)	0.0178	224768
UKBiobank+MVP	**−0.061(0.009)**	**0.0125**	**670128**



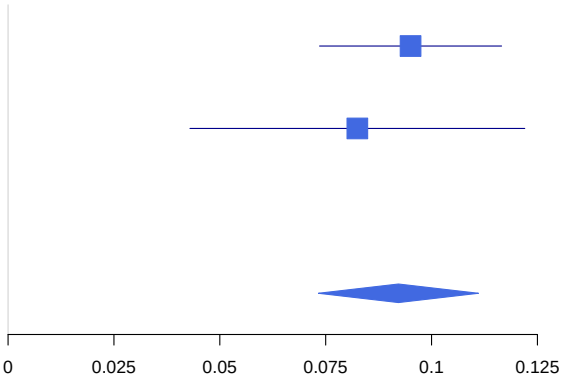
rs149165710, Effect allele/Other allele: A/G (PP)

Study	Beta(SE)	MAF	N
UKBiobank	0.138(0.02)	0.0033	445360
MVP	0.06(0.03)	0.0046	220163
UKBiobank+MVP	**0.115(0.016)**	**0.0037**	**665523**



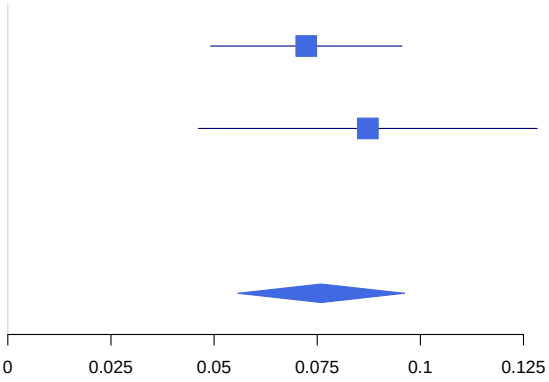
rs181200083, Effect allele/Other allele: C/A (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	0.095(0.011)	0.0094	445360
MVP	0.082(0.02)	0.0069	220501
UKBiobank+MVP	**0.092(0.01)**	**0.0088**	**665861**



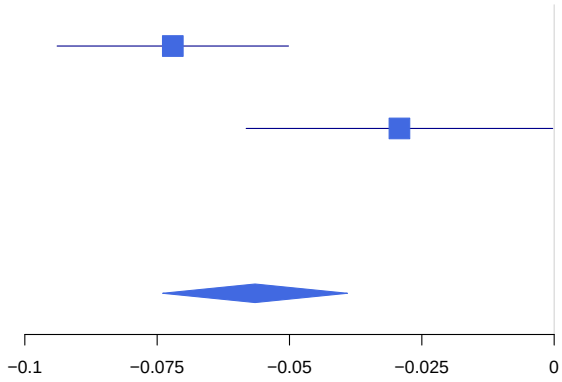
rs184289122, Effect allele/Other allele: G/A (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	0.072(0.012)	0.0084	445360
MVP	0.087(0.021)	0.0068	225112
UKBiobank+MVP	**0.076(0.01)**	**0.008**	**670472**



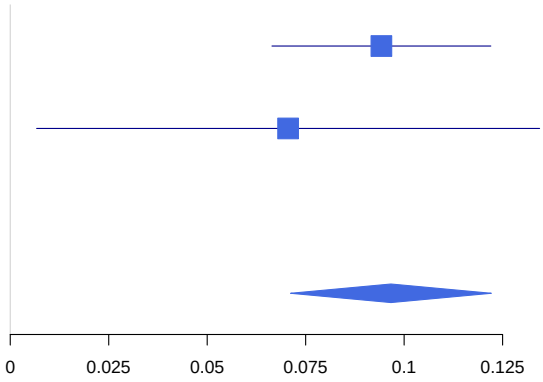
rs187207161, Effect allele/Other allele: C/T (PP)

Study	Beta(SE)	MAF	N
UKBiobank	−0.072(0.011)	0.0088	445360
MVP	−0.029(0.015)	0.0115	224770
UKBiobank+MVP	**−0.057(0.009)**	**0.0098**	**670130**



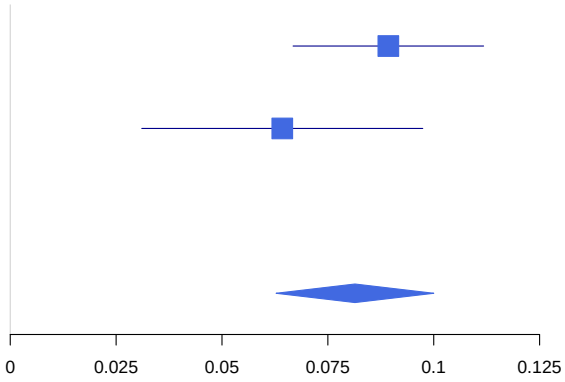
rs200383755, Effect allele/Other allele: C/G (DBP)

Study	Beta(SE)	MAF	N
UKBiobank	0.094(0.014)	0.006	445360
MVP	0.071(0.033)	0.004	225112
UKBiobank+MVP	**0.097(0.013)**	**0.0057**	**670172**



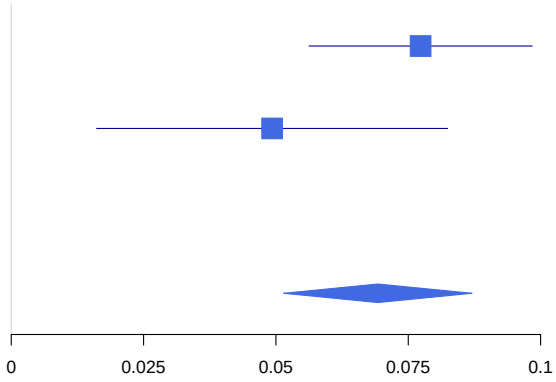
rs535313355, Effect allele/Other allele: C/T (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	0.089(0.011)	0.009	445360
MVP	0.064(0.017)	0.0082	225112
UKBiobank+MVP	**0.081(0.009)**	**0.0087**	**670472**



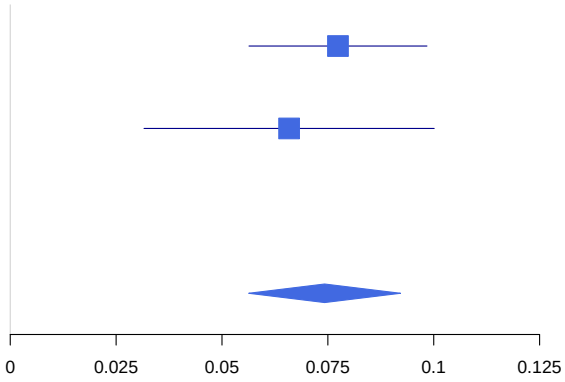
rs540369678, Effect allele/Other allele: T/A (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	0.077(0.011)	0.0095	445360
MVP	0.049(0.017)	0.0083	225112
UKBiobank+MVP	**0.069(0.009)**	**0.0092**	**670472**



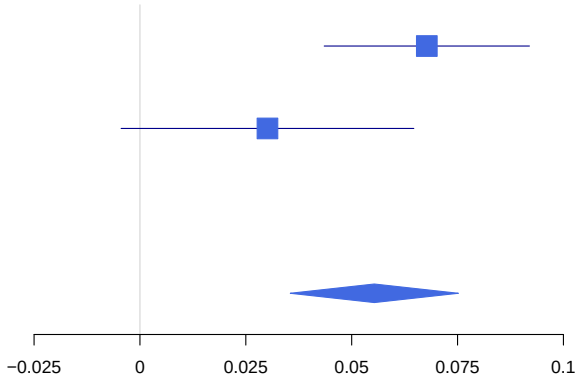
rs556058784, Effect allele/Other allele: G/A (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	0.077(0.011)	0.0095	445360
MVP	0.066(0.017)	0.0081	220501
UKBiobank+MVP	**0.074(0.009)**	**0.0091**	**665861**



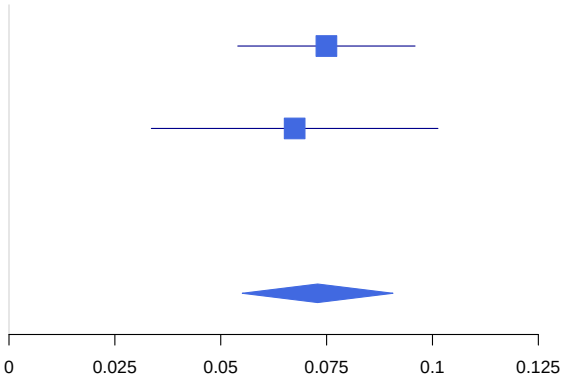
rs55833332, Effect allele/Other allele: G/C (PP)

Study	Beta(SE)	MAF	N
UKBiobank	0.068(0.012)	0.0082	445360
MVP	0.03(0.018)	0.0123	224769
UKBiobank+MVP	**0.055(0.01)**	**0.0095**	**670129**



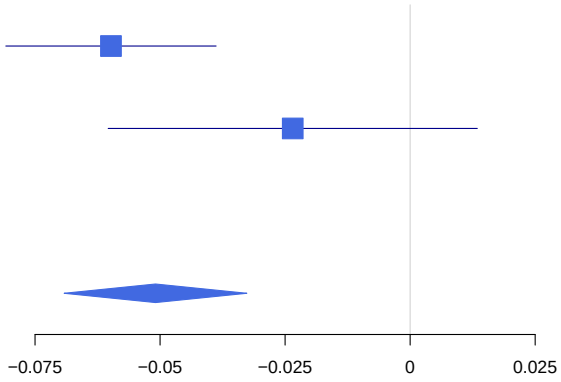
rs576629818, Effect allele/Other allele: T/C (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	0.075(0.011)	0.0094	445360
MVP	0.067(0.017)	0.0079	225112
UKBiobank+MVP	**0.073(0.009)**	**0.009**	**670472**



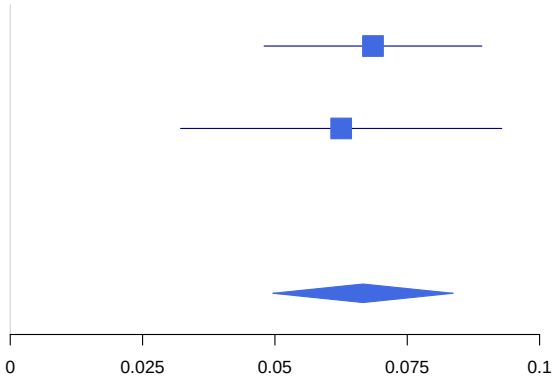
rs6061911, Effect allele/Other allele: C/T (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	−0.06(0.011)	0.0099	445360
MVP	−0.023(0.019)	0.0078	220501
UKBiobank+MVP	**−0.051(0.009)**	**0.0094**	**665861**



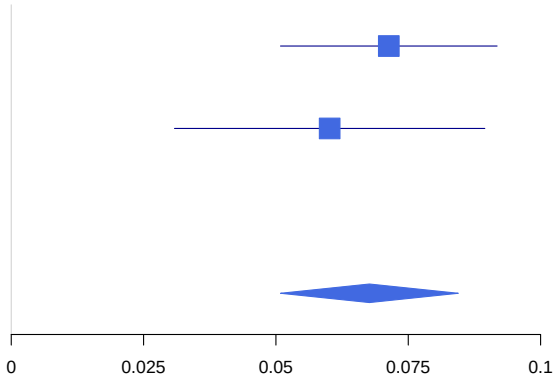
rs7076147, Effect allele/Other allele: G/A (SBP)

Study	Beta(SE)	MAF	N
UKBiobank	0.069(0.01)	0.0099	445360
MVP	0.063(0.015)	0.0105	225112
UKBiobank+MVP	**0.067(0.009)**	**0.0101**	**670472**



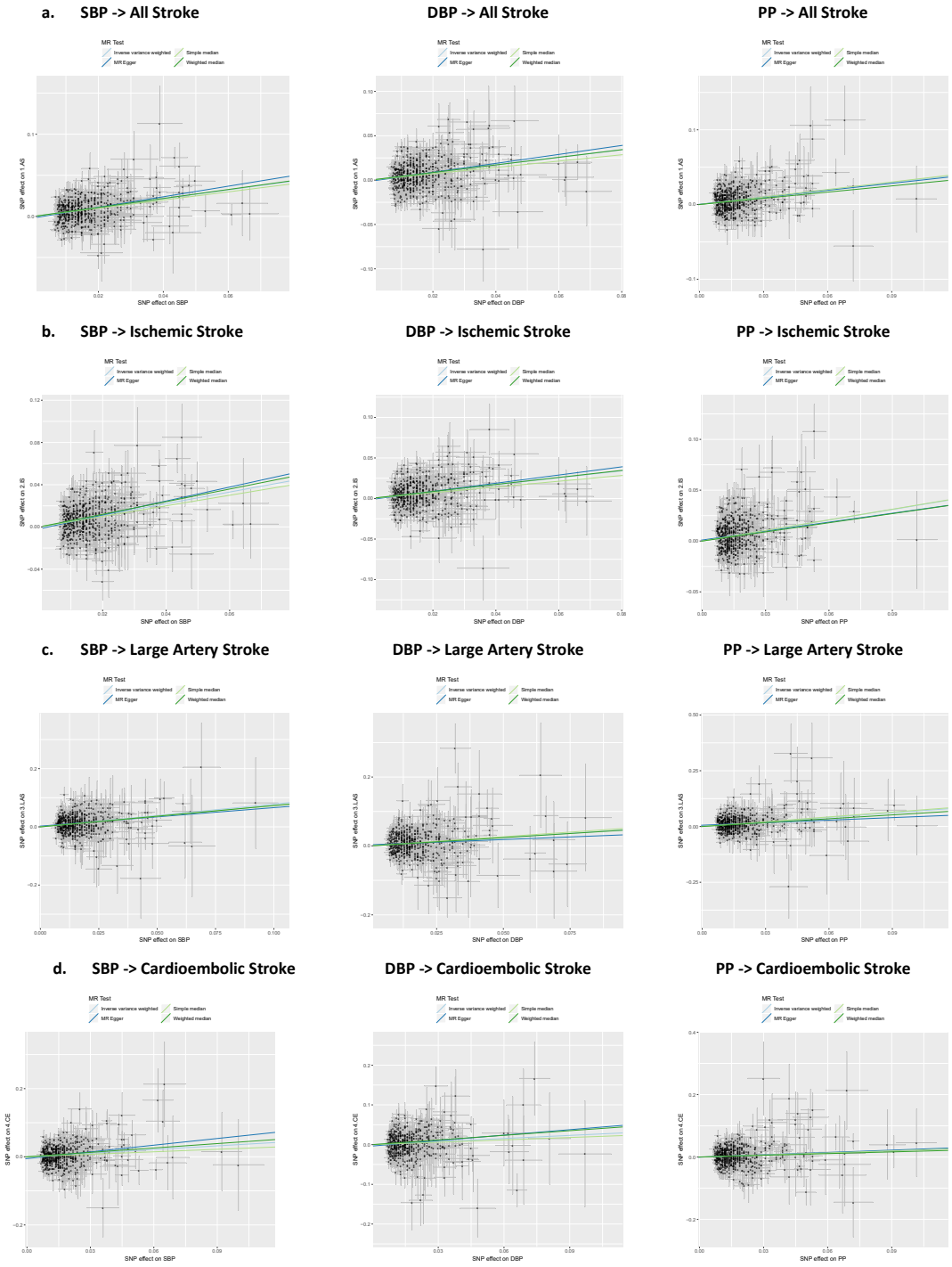
rs75337836, Effect allele/Other allele: T/G (SBP)

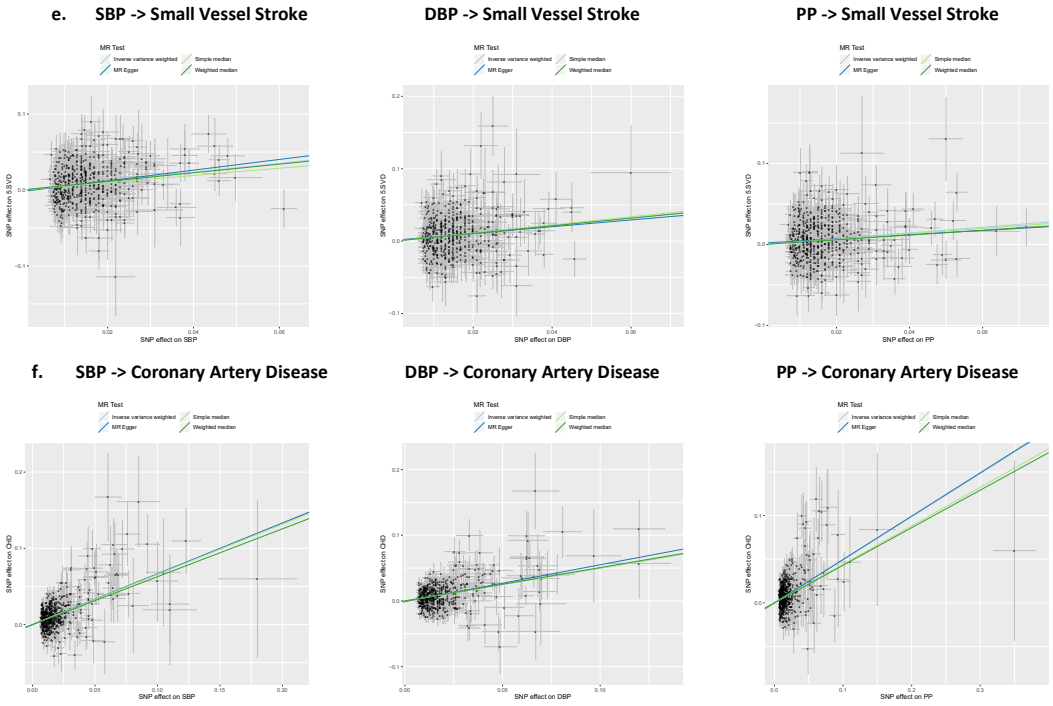
Study	Beta(SE)	MAF	N
UKBiobank	0.071(0.01)	0.0098	445360
MVP	0.06(0.015)	0.0105	225112
UKBiobank+MVP	**0.068(0.009)**	**0.0101**	**670472**



Presented are estimated transformed effect and 95% CI (Beta±1.96*SE).

Supplementary Figure 2. Mendelian randomization analysis for blood pressure level and risk of cardiovascular diseases.

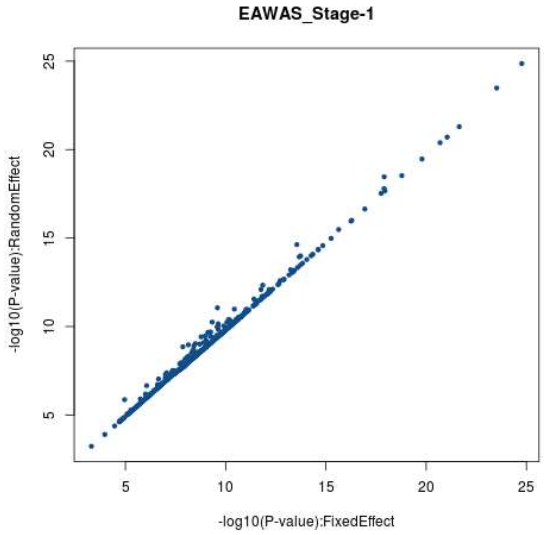




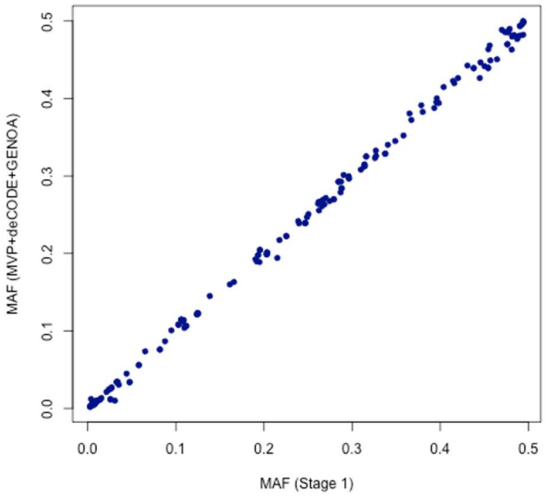
Associations between genetically determined blood pressure traits (SBP, DBP and PP) and risk of All Stroke (a), Ischemic Stroke (b), Large Artery Stroke (c), Cardioembolic Stroke (d), Small Vessel Stroke (e) and Coronary Artery Disease (f) based on four MR methods: IVW, MR-Egger, Simple median and Weighted median. Number of cases (N) - up to 122,733.

Supplementary Figure 3 (a) Comparison of the *P*-values for association of the novel BP SNVs from the random effects meta-analyses and the fixed effects meta-analyses as provided in Supplementary Table 2. -$\log_{10}$(*P*-values) are plotted. **(b)** Minor Allele Frequencies (MAF) of the novel BP-associations from Stage 1 of the EAWAS and the data request studies (MVP+deCODE+GENOA) restricted to EUR.

(a)

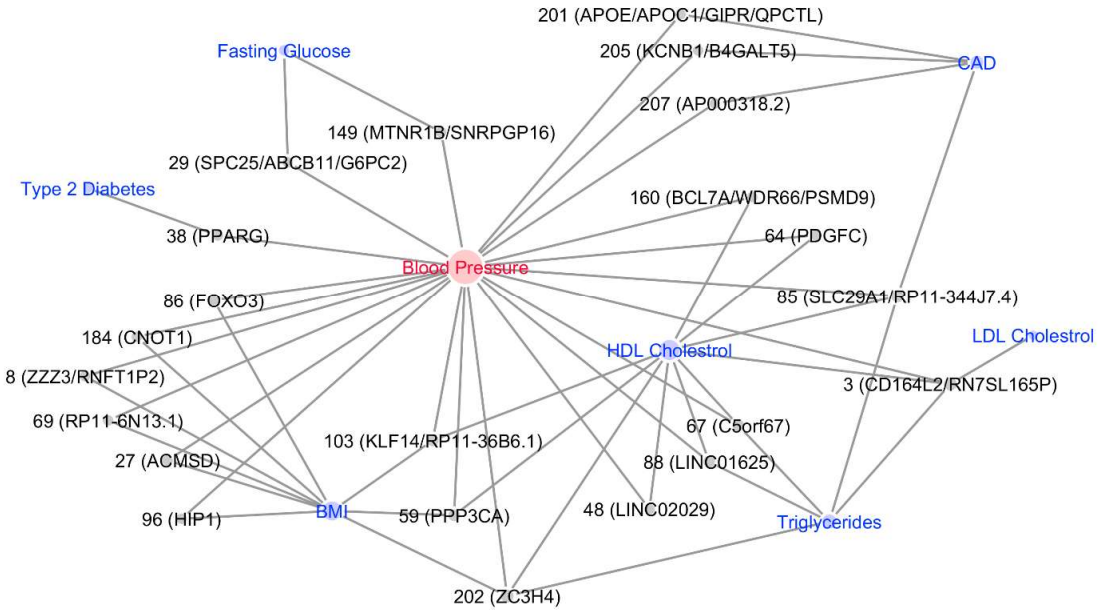


(b)



For each included variant, N is up to 864,822 participants in EAWAS Stage 1, and up to 448,666 participants in MVP+deCODE+GENOA.

Supplementary Figure 4. Co-localisation of the newly identified BP-associated loci with cardiometabolic traits using the UKBB GWAS data.



The locus number is provided for the novel locus with the nearest gene(s) in parentheses.

Supplementary Figure 5. Flowchart summarizing quality control procedures applied to genetic data in UKBB